

## **FIGURE 1**

GGGGCTTCGGCGCCAGCGGCCAGCGCTAGTCGGTCTGGTAAGGATTACAAAAGGTGCAGGTATG  
AGCAGGTCTGAAGACTAACATTGTGAAGTTGTAACAGAAAACCTGTTAGAAATGTGGTGGT  
TTCAGCAAGGCCTCAGTTCCCTTCAGCCCTGTAATTGGACATCTGCTGCTTCATATTT  
TCATACATTACTGCAGTAACACTCCACCATATAGACCCGGCTTACCTTATATCAGTGACACTGG  
TACAGTAGCTCCAGAAAAATGTTATTGGGGCAATGCTAAATATTGCGGCAGTTTATGCATTG  
CTACCAATTATGTTGTTATAAGCAAGTTCATGCTCTGAGTCCTGAAGAGAACGTTATCATCAA  
TTAAACAAGGCTGCCCTGTACTTGGAAACTTGAGTTAGGACTTCTATTGTGGCAAACCTT  
CCAGAAAACAACCCCTTTGCTGCACATGTAAGTGGAGCTGTGCTTACCTTGGTATGGCTCAT  
TATATATGTTGTTCAAGACCATCCTTCTACCAAATGCAGCCAAAATCCATGGCAAACAAGTC  
TTCTGGATCAGACTGTTGTTGTTATCTGGTGTGGAGTAAGTCACCTAGCATGCTGACTTGCTC  
ATCAGTTTGCAAGTGGCAATTGGGACTGATTTAGAACAGAAACTCCATTGGAACCCCGAGG  
ACAAAGTTATGTGCTTCACATGATCACTACTGCAGCAGAATGGCTATGTCAATTCTCTTT  
GGTTTTCTGACTTACATTGATTTCAAGAAAATTCTTACGGGTGGAAGCCAATTACA  
TGGATTAACCCCTATGACACTGCACCTTGCCTATTAAACAATGAACGAACACGGCTACTTCCA  
GAGATATTTGATGAAAGGATAAAATTTCTGTAATGATTGATTCTCAGGGATTGGGAAAGG  
TTCACAGAAGTTGCTTATTCTCTCTGAAATTCAACCACTTAATCAAGGCTGACAGTAACACT  
GATGAATGCTGATAATCAGGAAACATGAAAGAACGCCATTGATAGATTATTCTAAAGGATATCAT  
CAAGAAGACTATTAAAAACACCTATGCCTATACTTTTATCTCAGAAAATAAAGTCAAAAGACT  
ATG

## **FIGURE 2**

<subunit 1 of 1, 266 aa, 1 stop

<MW: 29766, pI: 8.39, NX(S/T): 0

MWWFQQGLSFLPSALVIWTSAAFIFSYITAVTLHHIDPALPYISDTGTVAPEKCLFGAMLNIAAV  
LCIATIYVRYKQVHALSPEENVIIKLNKAGLVLGILSCLGLSIVANFQKTTLFAAHVSGAVLTFG  
MGSLYMFVQTILSYQMOPKIHGKQVFIRLLLVIWCGVSALSMLTCSSVLHSGNFGTDLEQKLHW  
NPEDKGYVLHMITTAAEWSMSFSFFGFFLTYIRDQKISLRVEANLHGLTLYDTAPCPINNERTR  
LLSRDI

**Important features:**

**Type II transmembrane domain:**

amino acids 13-33

**Other Transmembrane domains:**

amino acids 54-73, 94-113, 160-180, 122-141

**N-myristylation sites.**

amino acids 57-63, 95-101, 99-105, 124-130, 183-189

### **FIGURE 3**

CGGACGCGTGGCGGACGCGTGGGGAGAGCCGCAGTCCCGCTGCAGCACCTGGAGAAGGCAGACC  
GTGTAGGGGGCCTGTGGCCCGAGCGTGTGGCTCGGGAGTGGAGTGGAGGAGGCCTC  
CTTACACTCGCCTGAGTTCTCATCGACTCCAGCATCATGATTACCTCCCAGATACTATTTTG  
GATTGGGTGGCTTTCTCATCGCCAATTGTTAAAGACTATGAGATACTGTCAGTATGTTGACAG  
GTGATCTTCTCGTGTGACGTTGACATTTCTGCACCATGTTGAGCTCATCATCTTGAAATCTTAGG  
AGTATTGAATAGCAGCTCCGTTATTCACTGGAAAATGAACCTGTGTGAAATTCTGCTGATCTGG  
TTTCATGGTGCCTTTTACATTGGCTATTGAGCAATATCCGACTACTGCATAAACACGA  
CTGCTTTTCTGTCTTTATGGTGTGACCTTATGTTCTTGAAACTAGGAGATCCCTTCC  
CATTCTCAGCCAAAACATGGGATCTTATCCATAGAACAGCTCATCAGCCGGTTGGTGTGATTGGAG  
TGACTCTCATGGCTTCTTCTGGATTGGTGTCACTGCCATACACTTACATGCTTACTTC  
CTCAGGAATGTGACTGACACGGATATTCTAGCCCTGGAACGGCAGTGTGCAAACCATGGATATGAT  
CATAAAGAAAAAGAAAAGGATGGCAATGGCACGGAGAACAAATGTTCCAGAAGGGGAAGTGCATAACA  
AACCATCAGGTTCTGGGAATGATAAAAGTGTACCTCAGCATCAGGAAGTGAATCTTACT  
CTTATTCAACAGGAAGTGGATGCTTGGAAAGAATTAGCAGGCAGCTTCTGAAACAGCTGATCT  
ATATGCTACCAAGGAGAGAATAGAAACTCCAAACCTCAAGGGAAATATTTAATTCTGGTT  
ACTTTTCTCTATTACTGTGTTGGAAAATTTCATGGCTACCACATCAATATTGTTTGATCGAGTT  
GGGAAAACGGATCTGTACAAGAGGCATTGAGATCACTGTGAATTATCTGGGAATCCAATTGATGT  
GAAGTTGGTCCAACACATTCTTCAATTGTTGAAATCATCGTCACATCCATCAGAGGAT  
TGCTGATCACTTACCAAGTTCTTATGCCATCTCTAGCAGTAAGTCCTCAATGTCATTGCTCTG  
CTATTAGCACAGATAATGGCATGTACTTGTCTCTGTGCTGATCCGAATGAGTATGCCTT  
AGAATACCGCACCATAATCACTGAAGTCCTGGAGAACACTGCAACTTCTATCACCGTGGTTG  
ATGTGATCTCCTGGTCAGCGCTCTCTAGCATACTCTCTCTATTGGCTCAAAACAGGCACCA  
GAGAAGCAAATGGCACTGACTTAAGCCTACTACAGACTGTTAGAGGCCAGTGGTTCAAAATTAA  
GATATAAGAGGGGGAAAATGGAACCAGGGCTGACATTATAAACAAACAAAATGCTATGGTAGC  
ATTTCACCTTCATAGCATACTCCTCCCGTCAGGTGATACTATGACCATGAGTAGCATCAGCCAG  
AACATGAGAGGGAGAGAACTAACTCAAGACAATACTCAGCAGAGAGCATCCGTGTGGATATGAGGCTGG  
TGTAGAGGCCAGAGGAGCCAAGAAACTAAAGGTGAAAATACACTGGAACCTGGCAAGACATGT  
CTATGGTAGCTGAGCCAAACAGCTAGGATTCCGTTTAAGGTTCACATGGAAAAGGTTAGCTT  
CCTTGAGATTGACTCATTAAATCAGAGACTGTAACAAAAAAAAAAAAAGGGCGCCGCG  
ACTCTAGAGTCGACCTGCAGAAGCTGGCCGCAACTTGTTATTGCAGCTATAATG

## **FIGURE 4**

MSFLIDSSIMITSQILFFGFGWLFFMRQLFKDYEIRQYVVQVIFSVTFAFSCTMFELIIFEILGV  
LNSSSRYFHWKMNLCVILLILVFMVPFYIGYFIVSNIRLLHKQRLLFSCLLWLTMYFFWKLGDP  
FPILSPKHGILSIEQLISRGVIGVTLALLSGFGAVNCPTYMSYFLRNVTDTDILALERLLQ  
TMDMIISKKKRMAMARRTMFQKGEVHNKPSPFWGMIKSVTTSASGSENLTLIQQEVDALEELSQR  
LFLETADLYATKERIEYSKTFKGKYFNFLGYFFSIYCWKIFMATINIVFDRVKGKTDPVTRGIEI  
TVNYLGIQFDVKFWSQHISFILVGIIIVTSIRGLLITLTKFFYAISSSKSSNVIVLLAQIMGMY  
FVSSVLLIRMSMPLERYRTIITEVILGELQFMFYHRWFDVIFLVSALSSILFLYLAHKQAPEKOMAP

**Important features:**

**Signal peptide:**

amino acids 1-23

**Potential transmembrane domains:**

amino acids 37-55, 81-102, 150-168, 288-311, 338-356, 375-398,  
425-444

**N-glycosylation sites.**

amino acids 67-70, 180-183 and 243-246

**Eukaryotic cobalamin-binding proteins**

amino acids 151-160

## FIGURE 5

AGCAGGGAAATCCGGATGTCCTGGTTATGAAGTGGAGCAGTGAGTGTGAGCCTAACATAGTTCC  
AGAACTCTCCATCCGGACTAGTTATTGAGCATCTGCCCTCATATCACCAAGTGGCCATCTGAGGT  
GTTTCCCTGGCTCTGAAGGGGTAGGCACGATGCCAGGTGCTTCAGCCTGGTGTGCTTCTCACT  
TCCATCTGGACCACGAGGCTCTGGTCAAGGCTTTGCGTGAGAAGAGCTTCCATCCAGGT  
GTCATGCAGAATTATGGGATCACCTTGTGAGCAAAAAGGCGAACCAAGCAGCTGAATTTCACAG  
AAGCTAAGGAGGCTGTAGGCTGCTGGGACTAAGTTGGCGGCAAGGACCAAGTTGAAACAGCC  
TTGAAAGCTAGTTGAAACTTGAGCTATGGCTGGGGATGGATTGCGTGCATCTAG  
GATTAGCCAAACCCCAAGTGTGGAAAATGGGTGGGTGCTGATTTGGAAGGTTCCAGTGA  
GCCGACAGTTGAGCTTACGCTATTGTTACAACACTCATCTGATACTTGACTAACTGTGCATTCCAGAA  
ATTATCACCAACCAAAAGATCCCATATTCAACACTCAAACACTGCAACACAAACACAAGAAATTATTGT  
CAGTGACAGTACCTACTCGGGCATCCCCCTACTCTACAATACCTGCCCTACTACTACTCCTC  
CTGCTCCAGCTTCACTTCTATTCCACGGAGAAAAAAATTGATTGTCAGAGAAGTTTATG  
GAAACTAGCACCAGTCTACAGAAACTGAACCATTGTTGAAAAATAAAGCAGCATTCAAGAATGA  
AGCTGCTGGTTGGAGGTGCCCCACGGCTCTGCTAGTGCTGCTCTTCTTTGGTGTG  
CAGCTGGTCTGGATTGCTATGTCAGGAGGTTACAGGAGGAGAAGGCCAATGATAGCAACCTAA  
CAGCAGAAGGAAATGATCGAAACCAAAAGTAGTAAAGGAGGAGAAGGCCAATGATAGCAACCTAA  
TGAGGAATCAAAGAAAATGATAAAAACCCAGAAGAGTCCAAGAGTCCAAGCAAACACTACCGTGC  
GATGCTGGAAGCTGAAGTTAGATGAGACAGAAATGAGGAGACACACCTGAGGCTGGTTCTT  
CATGCTCTTACCTGCCCCAGCTGGGAAATCAAAGGGCCAAGAACCAAAGAACAGAAAGTCCA  
CCCTGGTTCTTAACGGAAATCAGCTCAGGACTGCCATTGGACTATGGAGTGCAACCAAGAGAAAT  
GCCCTCTCTTATTGTAACCCGTCTGGATCCTATCCTCTACCTCCAAAGCTCCACGCC  
TTCTAGCCTGGTATGCTCTAATAATATCCCACGGAGAAAGGAGTTTGCAAAGTGAAGGAC  
CTAAAACATCTCATCAGTATCCAGTGGTAAAAGGCCCTGGTGTGAGGCTAGGTGGTTG  
AAAGCCAAGGAGTCACTGAGACCAAGGCTTCTACTGATTCGGCAGCTCAGACCCCTTCTCA  
GCTCTGAAAGAGAAACACGTATCCCACCTGACATGTCCTCTGAGCCGGTAAGAGCAAAAGAAT  
GGCAGAAAAGTTAGCCCCCTGAAAGCCATGGAGATTCTCATAACTTGAGACCTAATCTGTAAA  
GCTAAAATAAGAAAATGAAACAAGGCTGAGGATACGACAGTACACTGTCAGCAGGACTGTAAAC  
ACAGACAGGGTCAAAGTGTCTCTGAACACATTGAGTTGGAATCACTGTTAGAAACACACACA  
CTTACTTTCTGGTCTCTACCACTGCTGATATTCTCTAGGAAATATACTTTACAAGTAACA  
AAAATAAAAATCTTATAAATTCTATTCTATCTGAGTTACAGAAATGATTACTAAGGAAGATT  
ACTCAGTAATTGTTAAAAGTAATAAAATTCAACAAACATTGCTGAATAGCTACTATATGTC  
AAAGTGTGTGCAAGGTATTACACTCTGTAATTGAATATTATTCTCTAAAAAATTGACATAGTAG  
AACGCTATCTGGGAAGCTATTCTCTGAGTTGATATTCTAGCTTATCTACTTCCAAACTAAT  
TTTATTCTCTGAGACTAATCTTATTCTAATATGGCAACCATTATAACCTTAAATT  
TATTATTAACACCTAAGAAGTACATTGTTACCTATATACCAAAAGCACATTAAAAGTGC  
ATTAACAAATGTATCACTAGCCCTCTTTCCAACAAGAAGGGACTGAGAGATGCAGAAATT  
TGTGACAAAAAATTAAAGCATTAGAAAACCTT

## **FIGURE 6**

MARCFSLVLLTSIWTRLLVQGSLRAEELSIQVSCRIMGITLVSKKANQQLNTEAKEACRLLG  
LSLAGKDQVETALKASFETCSYGVGDGFVVISRISPNNPKCGKNGGVLIWKVPSRQFAAYCYN  
SSDTWTNSCIPEIITTKDPIFNTQTATQTTEFIVSDSTYSVASPYSTIPAPTTPPAPASTSIPR  
RKKLICVTEVFMETSTMSTETEPFVENKAASKNEAAGFGGVPTALLVLALLFFGAAAGLGFCYVK  
RYVKAFPFTNKNQQKEMIETKVVKEEKANDSNPNEESKTDKNPEESKSPSKTTVRCLEAEV

**Signal sequence:**

amino acids 1-16

**Transmembrane domain:**

amino acids 235-254

**N-glycosylation site.**

amino acids 53-57, 130-134, 289-293

**Casein kinase II phosphorylation site.**

amino acids 145-149, 214-218

**Tyrosine kinase phosphorylation site.**

amino acids 79-88

**N-myristoylation site.**

amino acids 23-29, 65-71, 234-240, 235-239, 249-255, 253-259

## **FIGURE 7**

CGCCCGCCTCCGCACCCGCGCCCGCCCACCGCGCCGCTCCCGCATCTGCACCCGCAGCCCGGC  
GGCCTCCCGCGGGAGCGAGCAGATCCAGTCGGGCCCCGAGCGCAACTCGGTCCAGTCGGGGCGG  
CGGCTCGGGCGCAGAGCGGAGATGCAGCGGCTTGGGGCACCCCTGCTGTGCCCTGCTGCG  
CGCGGTCCCCACGGCCCCCGCGCCGCTCGACGGCACCTCGGTCCAGTCAGAAGCCGGCC  
GCTCTAGCTACCCGAGGAGGCCACCTCAATGAGATGTCAGGAGGTTGAGGAACAGT  
GGAGGACACGACAAATTGCGCAGCGCGTGGAAAGAGATGGAGGCAGAAGAAGCTGCTGCTA  
AACATCATCAGAAGTGAACCTGGCAAACCTACCTCCAGCTATCACAATGAGACCAACACAGAC  
ACGAAGGTTGAAATAATACCATCCATGTGACCGAGAAATTCAAAAGATAACCAACAACAGAC  
TGGACAAATGGTCTTTCAAGAGACAGTTACATCTGAGGAGACGAAGAAGGCAGAAGGAGCC  
ACGAGTGCATCATCGACGAGGACTGTGGGGCCAGCATGTAAGTGCAGTTGCCAGCTCCAGTAC  
ACCTGCCAGCCATGCCGGGGCCAGAGGATGCTCTGCACCCGGGACAGTGAGTGTGAGGACCA  
GCTGTGTCTGGGTCACTGCACCAAAATGGCCACCAGGGGAGCAATGGGACCATCTGTGACA  
ACCAGAGGGACTGCCAGCGGGCTGTGTGCTGCCAGAGAGGCCTGCTGTTCCAG  
ACACCCCTGCCGTGGAGGGCGAGCTTGCATGACCCCGCCAGCCGGCTTCTGGACCTCATCAC  
CTGGGAGCTAGAGCCTGATGGAGCCTGGACCGATGCCCTGTGCAAGTGGCAGTGGCCTCCTGCG  
CCCACAGCCACAGCCTGGTGTATGTGCAAGCCGACCTCGTGGGAGGCCGTGACCAAGATGG  
GAGATCCTGCTGCCAGAGAGGTCCCCGATGAGTATGAAGTGGCAGCTCATGGAGGAGGTGCG  
CCAGGAGCTGGAGGACCTGGAGAGGAGCCTGACTGAAGAGATGGCCTGGGGAGCCTGCG  
CCGCGCTGCACTGCTGGGAGGGAGAGATTAGATCTGGACCGCTGTGGTAGATGTGCAA  
TAGAAATAGCTAATTATTCCCCAGGTGTGCTTGGCGTGGCTGACCAGGTTCTTCTA  
CATCTCTCCCAGTAAGTTCCCCTGTGCTTGACAGCATGAGGTGTGCAATTGTTCAAGCT  
CCCCCAGGCTGTTCTCCAGGCTTCACAGTCTGGTGTGCTGGAGAGTCAGGCAGGGTAAACTGCA  
GGAGCAGTTGCCACCCCTGTCAGATTATTGGCTGCTTGCCTCTACCAAGTGGCAGACAGCCG  
TTTGTCTACATGCTTGTATAATTGTTGGAGGGAGGAGATGAAACAAATGAGTCTCCCTC  
TGATTGGTTGGGAAATGAGAGTGCCTGCTTGCAACATCAACCTGGAAAAATG  
CAACAAATGAATTTCACGCAGTCTTCCATGGCATAGGTAAGCTGTGCCCTCAGCTGTTGC  
AGATGAAATGTTCTGTTCACCTGCATTACATGTGTTATTCACTCCAGCAGTGTGCTCAGCTCC  
TACCTCTGTGCCAGGGCAGCATTTCATATCCAAGATCAATTCCCTCTCAGCACAGCCTGGG  
AGGGGGCATGTTCTCTCGCCATCAGGGATCTCAGAGGCTCAGAGACTGCAAGCTGCTGCC  
CAAGTCACACAGCTAGTGAAGACCAGAGCAGTTCATCTGGTGTGACTCTAACGCTAGTGC  
CTCCACTACCCACACCAGCCTGGTGCACCAAAAGTGTCTCCCAAAAGGAAGGAGAATGGGAT  
TTTCTTGAGGCATGCACATCTGAAATTAGGTCAAACATAATTCTCACATCCCTCTAAAGTAA  
CTACTGTTAGGAACAGCAGTGTCTCACAGTGTGGGAGCCGCTTCTAATGAAGACAATGAT  
ATTGACACTGTCCTCTTGGCAGTTGCAATTAGTAACCTTGAAAGGTATATGACTGAGCGTAGCA  
TACAGGTTAACCTGCAGAAACAGTACTTAGGTAAATTGTAGGGCAGGGATTATAATGAAATTGCA  
AAAATCACTTAGCAGCAACTGAAGACAATTATCAACCACTGGAGGGAAATCAAACCGAGCAGGGC  
TGTGTGAAACATGGTGTAAATATGCGACTGCGAACACTGAACCTACGCCACTCCACAAATGATG  
TTTCAGGTGTCTGGACTGTTGCCACCATGTATTCACTCCAGAGTCTTAAAGTTAAAGTTGCA  
CATGATTGTATAAGCATGCTTCTTGAGTTAAATTATGTATAAACATAAGTTGCATTAGAA  
ATCAAGCATAAAATCACTCAACTGCAAAAAAAAAAAAAAA

## **FIGURE 8**

MQRLGATLLCLLLAAAVPTAPAPAPTATSAPVKPGPALSYPQEEATLNEMFREVEELMEDTQHKL  
RSAVEEMEAAKASSEVNLNLPPSYHNETNTDTKGNNTIHVHREIHKITNNQTGQMVFSE  
TVITSGVDEEGRSHECIIDEDCGPSMYCQFASFQYTCOPCRGQMLCTRSECCGDQLCVWGHC  
TKMATRGSNGTICDNQRDCQPGLCCAFQRGLLFPVCTPLPVEGELCHDPASRLLLITWELEPDG  
ALDRCPASCAGLLCQPHSHSLVYVCKPTFVGSRDQDGEILLPREVPDEYEVGSFMEEVROELEDLE  
RSLTEEMALGEPAAAAALLGGEI

**Signal sequence:**

amino acids 1-19

**N-glycosylation site.**

amino acids 96-100, 106-110, 121-125, 204-208

**Casein kinase II phosphorylation site.**

amino acids 46-50, 67-71, 98-102, 135-139, 206-210, 312-316,  
327-331

**N-myristoylation site.**

amino acids 202-208, 217-223

**Amidation site.**

amino acids 140-144

## **FIGURE 9**

CGGACCGTGGCGGACCGTGGGGCTGTGAGAAAGTCCAATAAACATCATGCAACCCAC  
GGCCACCTTGTGAACCTCGTGCCTCAGGGCTATGTGCGTCTTCAGGGCTACTCATCCAAAG  
GCCTAATCCAACGTTCTGCTTCATCTGAAATCTATGGGTCTGGGCTCTCTGGACCCCTT  
AACTGGGTACTGGCCCTGGCCAATGCGTCTCGCTGGAGCCTTGCCTCCTACTGGCCTT  
CCACAAGCCCCAGGACATCCCTACCTCCCCCTAATCTCTGCCTTCATCCGCACACTCCGTTAC  
ACACTGGGTACTGGCATTGGCATTGGAGCCCTACCTGACCCCTGTGCAGATAGCCGGTCACTTTG  
GAGTATATTGACCACAAGCTCAGAGGAGTCAGAACCCTGTAGCCGCTGCATCATGTGCTGTTT  
CAAGTGCTGCCTCTGGTGTCTGGAAAAATTATCAAGTCTAAACCGCAATGCATACATCATGA  
TCGCCATCTACGGGAAGAATTCTGTGTCTCAGCCAAAATGCGTTCATGCTACTCATGCGAAAC  
ATTGTCAAGGGTGGTGTCTGGACAAAGTCACAGACCTGCTGCTGTTCTTGGGAAGCTGCTGGT  
GGTCGGAGGCCTGGGGCTCTGCTCTCTCTCCGGTCGATCCGGGCTGGTAAAG  
ACTTTAAGAGCCCCACCTCAACTATTACTGGCTGCCATCATGACCTCCATCCTGGGGCTAT  
GTCATGCCAGCGCTCTTCAGCGTTTCGGCATGTGTGGACAGCCTCTCCCTCTGCTCT  
GGAAGACCTGGAGCGGAACAACGGCTCCCTGGACCGGGCTACTACATGTCCAAGAGCCTCTAA  
AGATTCTGGCAAGAAGAACGAGGCGCCCCGGACAACAAGAAGAGGAAGAAGTGACAGCTCCGG  
CCCTGATCCAGGACTGCACCCCCACCCCCACCGTCCAGCCATCCAACCTCACTTCGCTTACAGGT  
CTCCATTTGTGGTAAAAAAAGTTTAGGCCAGGCCTGGCTCACGCTGTAATCCAACACT  
TTGAGAGGCTGAGGCCTGGGCGGATCACCTGAGTCAGGAGTTGAGACCAGCCTGCCAACATGGTG  
AAACCTCCGTCTCTATTAAAAACAAAAATTAGCCGAGAGTGGTGCATGCACCTGTCACTCCA  
GCTACTCGGGAGGTGAGGCAGGGAGAATCGCTGAACCCGGAGGCAGAGGTTGCAGTGAGCCGA  
GATCGGCCACTGCACTCCAACCTGGGTGACAGACTCTGTCTCCAAAACAAAACAAACAAA  
AAGATTTATTAAAGATATTTGTTAACTC

## **FIGURE 10**

RTRGRTRGGCEKVPIINTSCNPTAHLVNSSCPGLMCVFQGYSSKGLIQRSVFNLQIYGVLGLFWTL  
NWVLALGQCVLAGAFASFYWAFHKPQDIPTFPLISAFIRTLYHTGSLAFGALILTLVQIARVIL  
EYIDHKLRGVQNPVARCIMCCFKCCLWCLEKFIKFLRNAYIMIAIYGKNFCVSAKNAFMLLMRN  
IVRVVVLDKVTDLFFFGLKLLVVGGVGVLSSSSSGRIPGLGKDFKSPHLNYYWLPIMTSILGAY  
VIASGFFSVFGMCVDTLFLCFLEDLERNNGSLDRPYYMSKSLLKILGKKNEAPPDNKKRKK

**Important features:**

**Transmembrane domains:**

amino acids 57-80 (type II), 110-126, 215-231, 254-274

**N-glycosylation sites.**

amino acids 16-20, 27-31, 289-293

**Hypothetical YBR002c family proteins.**

amino acids 276-288

**Ammonium transporters proteins.**

amino acids 204-231

**N-myristoylation sites.**

amino acids 60-66, 78-84

**Amidation site.**

amino acids 306-310

## **FIGURE 11**

CCCCCGCGCCCGGCCGGCGCCGGCGCCGAAGCCGGGAGCCACCGCCATGGGGGCTGCCTGGGAGCCTGC  
TCCCTGCTCAGCTGCGCGTCTGCCCTGCGCTCTGCCCTGCATCCGTGAGCTGCTGCCCGC  
CAGCCGCAACTCCACCGTGAGCCGCTCATCTTCACGTTCTCCCTTCTGGGTGCTGGTGTCCA  
TCATTATGCTGAGCCGGCGTGAGAGTCAGCTACAAGCTGCCCTGGGTGTTGAGGAGGGGCC  
GGGATCCCCACCGTCTGCAGGGCACATCGACTGTGGCTCCCTGCTGGCTACCGCGCTGTCTACCG  
CATGTGCTTCGCCACGGCGCTCTTCTTACCCCTGCTCATGCTCGGTGAGCAGCA  
GCCGGGACCCCGGGCTGCCATCCAGAATGGGTTGGTCTTAAGTCCGTATCCGTGGCTGGCCTC  
ACCGTGGGTGCCTTCTACATCCCTGACGGCTCCCTCACCAACATCTGGTCTACTTCGGCGTGTGGG  
CTCCTTCTCTTCATCCCTCATCCAGCTGGTGTGCTCATCGACTTGCCTACTGGAACCGCGGT  
GGCTGGGCAAGGCCGAGGAGTGCATTCCCGTGCCTGGTACGCAGGCCCTTCTTCACTCCCTC  
TTCTACTTGCTGTCGATCGGGCGTGGCGCTGATGTTCATGTAACACTGAGCCCAGCGGTGCCA  
CGAGGGCAAGGTCTTCATCAGCTCACCTCACCTCTGTGTCTGCGTGTCCATGCTGTCTGC  
CCAAGGTCCAGGACGCCAGCCAACTCGGGTCTGCTGCAGGCCCTGGTACACCCCTACACCATG  
TTTGTCACCTGGTCAGCCCTATCCAGTATCCCTGAACAGAAATGCAACCCCCATTGCCAACCCAGCT  
GGGCAACGAGACAGTTGTGGCAGGCCCGAGGGCTATGAGACCCAGTGGTGGATGCCCGAGCATTG  
TGGGCCCTCATCATCTTCTCTGTGACCCCTTCTCATCAGTCTGCGCTCCCTCAGACCCACGGCAGGTG  
AACAGCCTGATGCAACGGAGGTGCCACCTATGCTAGACGCCACACAGCAGCAGCAGCAGG  
GGCAGCCTGTGAGGCCGGCCTTGACAACGAGCAGGACGGCGTACCTACAGCTACTCCCTTCC  
ACTTCTGCCCTGGTGTGGCCTCACTGCACGTACATGATGACGCTCACCAACTGGTACAAGCCGGTGAG  
ACCCGGAAGATGATCAGCACGTGGACGCCGTGTGGGTGAAGATCTGTGCCAGTGGCAGGGCTGCT  
CCTCTACCTGTGGACCCCTGGTAGCCCCACTCCCTGCGCAACCGCGACTTCAGCTTGAGGCAGCCTCA  
CAGCCTGCCATCTGGTGCCTCTGCCACCTGGTGCCTCTGGCTCGGTACAGCCAACCTGCCCTC  
CCACACCAATCAGCCAGGCTGAGCCCCACCCCTGCCAGCTCCAGGACCTGCCCTGAGCCGGC  
CTTCTAGTCGTAGTGCCTCAGGGTCCGAGGAGCATCAGGCTCTGCAGAGCCCCATCCCCCGCCAC  
ACCCACACGGTGGAGGCTGCCCTCCCTCCCTGCCAGCTCCAGGACCTGCCCTGAGCCGGC  
AGGGCTCCCTGTCCCTCAGGCTCACGGGAGCGGGGCTGCTGGAGAGAGCGGGGAACTCCCACCA  
TGGGGCATCCGGCACTGAAGCCCTGGTGTTCCTGGTACAGTCCCCCAGGGACCCCTGCCCTTCTG  
GACTTCGTGCCTTACTGAGTCTAAGACTTTCTAATAAACAGCCAGTGCCTGTAAAAAAAAAA

## **FIGURE 12**

MGACLGACSLSCASCLCGSAPCILCSCCPASRNSTVSRLIFTFFLFLGVLVSIIMLSPGVESQL  
YKLPWVCEEGAGIPTVLQGHIDCGSLLGYRAVYRMCFATAAFFFFFTLLMLCVSSSRDPRAAIQ  
NGFWFFKFLILVGLTVGAFYIPDGSFTNIWFYFGVVGSFLFILIQLVLLIDFAHAWNQRWLKGAE  
ECDSRAWYAGLFFFLLFYLLSIAAVALMFYYTEPSGCHEGKVFISLNLTFCVCVSIAAVLPKV  
QDAQPNNSLLQASVITLYTMFTWSALSSIEQKCNPHLPTQLGNETVAGPEGYETQWWDAPSI  
VGLIIFLLCFLFISLRSSDHRQVNSLMQTEECPPMLDATQQQQQQVAACEGRAFDNEQDGVTYSY  
SFFHFCLVLASLHVMMTLTNWYKPGTRKMIWTAVWVKICASWAGLLYLWTLVAPLLLNRD  
FS

**Signal sequence:**

amino acids 1-20

**Transmembrane domains:**

amino acids 40-58, 101-116, 134-150, 162-178, 206-223, 240-257,  
272-283, 324-340, 391-406, 428-444

### **FIGURE 13**

CGGGCCAGCCTGGGGCGGCCAGGAACCACCCGTTAAGGTGTCTCTCTTAGGGATGGTGA  
GGTTGGAAAAAGACTCCTGTAACCCCTCCTCCAGGATGAACCACCTGCCAGAAGACATGGAGAACG  
CTCTCACCGGGAGCCAGAGCTCCATGCTCTGCGCAATATCCATTCCATCAACCCCACACAA  
CTCATGCCAGGATTGAGTCCTATGAAGGAAGGGAAAAGAAAGGCATATCTGATGTCAGGAGGAC  
TTTCTGTTGTTGTCACCTTGACCTTATTGTAACATTACTGTGGATAATAGAGTTAAATG  
TGAATGGAGGCATTGAGAACACATTAGAGAACGGAGGTGATGCAGTATGACTACTATTCTTCATAT  
TTTGATATATTCTCTGGCAGTTTCGATTTAAAGTGTAAACTTGCAATGCTGTGCGAG  
ACTGCGCCATTGGTGGCAATAGCGTTGACAACGGCAGTGACCAGTGCCCTTTACTAGCAAAAG  
TGATCCTTCGAAGCTTTCTCAAGGGGCTTTGGCTATGTGCTGCCATCATTCAATTCA  
CTTGCCCTGGATTGAGACGTGGTCCTGGATTCAAAGTGTACCTCAAGAACAGAGAACAGAAA  
CAGACTCCTGATAGTCAGGATGCTTCAGAGAGGGCAGCACTTACCTGGTGGCTTCTGATG  
GTCAGTTTATTCCCTCCTGAATCGAACAGCAGGATCTGAAGAACGCTGAAGAAAAACAGGACAGT  
GAGAAACCACTTAGAACACTATGAGTACTACTTTGTTAAATGTGAAAACCCCTCACAGAAAGTC  
ATCGAGGCACAAAGAGGCAGGCAGTGAGTCTCCCTGTCGACAGTAAAGTTGAAATGGTGACGTC  
CACTGCTGGCTTATTGAACAGCTAATAAAGATTATTGTAATACCTCACAAACGTTGAC  
CATATCCATGCACATTAGTGCCTGCCTGTCAGGTAAGGTAATGTCAATTGATTCAATTCT  
TCAGTGAGACTGAGCCTGATGTTAACAAATAGGTGAAGAACGCTTGTGCTGTATTCTAAC  
AAAAGACTTAATATATTGAAGTAACACTTTTTAGTAAGCAAGATACTTTTATTCAATTCA  
AGAATGGAATTTTTGTTCATGTCTCAGATTATTTGTATTCTTTAACACTCTACATT  
TCCCTGTTTTAACATGCACATGTGCTTTGCATTATGTTGATGGCTGAAGTGTGGA  
ACATGTCAATGTGGCTAGTTATTCTGTTGCATTATGTTGATGGCTGAAGTGTGGA  
CTTGCAAAAGGGGAAGAAAGGAATTGCGAACATGTAAGTCACTGGCAGACATTGATTATT  
TTATCATGAAATCATGTTCTGATTGTTCTGAAATGTTCTAAATACTCTTATTGAAATGC  
ACAAAATGACTAAACCATTCATATCATGTTCTTGCCTTCAGCCAATTCAATTAAAATGAA  
CTAAATTAAAAA

## **FIGURE 14**

MNHLPEDMENALTGSQSSHASLRNIHSINPTQLMARIESYEGREKKGISDVRRTFCLFVTFDLLF  
VTLLWIIELNVNGGIENTLEKEVMQYDYYSSYFDIFLLAVFRFKVLILAYAVCRLRHWWAIALTT  
AVTSAFLLAKVILSKLFSQGAFGYVLPIISFILAWIETWFLDFKVLPOEAEEENRLLIVQDASER  
AALIPGGLSDGQFYSPPESEAGSEEAEEKQDSEKPLLEL

**Important features of the protein:**

**Signal peptide:**

amino acids 1-20

**Transmembrane domains:**

amino acids 54-72, 100-118, 130-144, 146-166

**N-myristoylation sites.**

amino acids 14-20, 78-84, 79-85, 202-208, 217-223

## **FIGURE 15**

ACTCGAACGCAGTTGCTTCGGGACCCAGGACCCCCCTGGGGCCAGCCGAGAAAGACTGAGG  
CCGCAGGCTGCCCGCCGGCTCCCTGGCCGCCGCTCCGGACAGAACATGTGCTCCAG  
GGTCCCCTGCTGCTGCCGCTCTGCTACTGGCCCTGGGGCTGGGGCTGAGGGCTGCCAT  
CCGGCTGCCAGTGACGCCAGCACAGACAGTCTCTGCACTGCCCGCCAGGGACACGGTGC  
CGAGACGTGCCACCCGACACGGTGGGCTGTACGTCTTGAGAACGGCATCACCATGCTGACGC  
AGGCAGCTTGGCCCTGGCCCTGCACTCTGGACCTGTACAGAACAGATGCCAGCC  
TGCCCAGCGGGCTTCCAGCACTGCCAACCTCAGAACCTGGACCTGACGCCAACAGGCTG  
CATGAAATACCAATGAGACCTCCGTGGCTGCGCCTCGACACGCTGACGCCCTGGAGCTAAGCTGC  
CCGCATCCGCACATCCAGCTGGTGCCTCGACACGCTGACGCCCTGGAGCTAAGCTGC  
AGGACAACGAGCTGCCGGACTGCCCGCTGCGCCTGCCCGCTGCTGCTGGACCTCAGC  
CACAAACAGCCTCTGGCCCTGGAGCCGGCATCTGGACACTGCCAACGTGGAGGCGCTGGC  
GGCTGGCTGGGGCTGCAAGCAGCTGGACGAGGGCTCTCAGCCGTTGCGAACCTCCAGGACC  
TGGATGTGTCCGACAACCAGCTGGAGCGAGTGCACACTGGCAGCCCTGAGGAGACGCGTGC  
CGCCTGCGGCTGGCCGGAACACCCGATTGCCAGCTGCCGGAGGACCTGGCGGCGCTGGC  
TGCCCTGCAAGGAGCTGGATGTGAGCAACCTAAGCCTGAGGCCCTGGCGACCTCTGGGCC  
TCTTCCCCCGCTGCGGCTGCTGGCAGCTGCCGCAACCCCTCACTGCGTGTGCCCTGAGC  
TGGTTGGCCCTGGGTGCGCAGAGGCCACGTCACACTGGCAGCCCTGAGGAGACGCGTGC  
CTTCCCAGCAAGAACGCTGGCCGGCTGCTCTGGAGCTGACTACGCCGACTTTGGCTGCCAG  
CCACCAACACCACAGCCACAGTGCCAACACAGGAGCCGGTGGTGGGGAGGCCACAGCCTTGCT  
TCTAGCTTGGCTCTACCTGGCTAGCCCCACAGGCCGGCAACTGAGGCCCCAGGCCACCTG  
CACTGCCCAACCGACTGTAGGGCTGTCCCCAGCCCCAGGACTGCCACCGTCCACCTGCC  
ATGGGGCACATGCCACCTGGGACACGGGACCCATGGCGTGTGCTGTGCCCGAAGGCTTCACG  
GGCCTGTACTGTGAGAGCCAGATGGGGACAGGGCCAGGCCCTACACCAGTCAGCCGAG  
GCCACACGGTCCCTGACCCCTGGCATCAGGCCGGTGAAGGCCACCTCCCTGCCGTGGGCTG  
AGCGTACCTCCAGGGGAGCTCCGTGCACTCAGGAGCCCTCCGTCTCACCTATGCAACCTATCG  
GGCCTGATAAGGGCTGGTGAAGCTGCCACTGCTGCTCATGCCCTGGGCCGGGGTGGGAGG  
GCGAGGAGGCCCTGGGGAGGGCATAACCCCCAGGCCCTGCCACTCCATGCCGCGGTGCTCC  
CAGGCCCGAGGGCAACCTGCCGCTCTCATGCCGCGGTGCTGCCGCGGTGCTCC  
GCTGGCTGCCGAGGGCAGCTGGGGCTCTGGAAGTGGAGGAGTGAAGGTCCCCCTGGAG  
ACAAAGGGCAGGTGGGGCAGGGCTGGGGCTGGAAGTGGAGGAGTGAAGGTCCCCCTGGAG  
CCAGGGCGAAGGAACAGAGGGCGGTGGAGAGGCCCTGCCAGGGGTCTGAGTGTGAGGTGCC  
ACTCATGGCTTCCCTGGCCCTGGCCTCCAGTCACCCCTCCACGCAAAGCCCTACATCTAAGCCA  
GAGAGAGACAGGGCAGTGGGGCGGCTCTGAGCCAGTGAAGATGCCAGCCCCCTGCTGCC  
ACACCACTAAGTCTCAGTCCAACCTGGGATGTGCAAGACAGGGCTGTGACCAACAGCT  
GGGCCCTGTTCCCTGGACCTGGCTCTCATCTGTGAGATGCTGTGCCAGCTGACGAGCC  
CTAACGTCCCCAGAACCGAGTGCCTATGAGGACAGTGTCCGCCCTGCCAACGTGCAAGTC  
CCTGGGCAAGGCCGGCCCTGCCATGTGCTGGTACGCAATGCCCTGGGTCTGCTGGGCTCT  
TCCAGGCCGAGCCCTGGGGCCAGTGAAGGAAGCTCCGGAAAGAGCAGAGGGAGAGCGGGTAGGC  
GGCTGTGTGACTCTAGTCTTGGCCCCAGGAAGCGAAGGAACAAAAGAAACTGGAAGGAAGATGC  
TTTAGGAACATGTTTGTCTTTAAATATATATTTATAAGAGATCCTTCCCATTATCT  
GGGAAGATGTTTCAAAACTCAGAGACAAGGACTTGGTTTGTAAGACAAACGATGATATGAA  
GGCTTTGTAAGAAAAATAAAAGATGAAGTGTGAA

## **FIGURE 16**

MCSRVPLLLPLLLLALGPGVQGCPSCQCSQPQTVFCTARQGTTVPRDVPPDTVGLYVFENGIT  
MLDAGSFAGLPGLQQLLDSLQNQIASLPSGVFQPLANLSNLDLTANRLHEITNETFRGLRRLERLY  
LGKNRIRHIQPGAFDTLDRLLLEKLQDNELRALPPLRIPRLLLLLDSHNSLLALEPGILDtanve  
ALRLAGLGLQQLDEGLFSRLRNLHLDLVDNQLERVPPVIRGLRGLTRLRLAGNTRIAQLRPEDL  
AGLAALQELDVSNLSQLPGDLSGLFPRLLAARNPNCVCPLSWFGPWVRESHVTLASPEE  
TRCHFPPKNAGRLLLEDYADFGCPATTTATVPTTRPVVREPTALSSSLAPTWLSPTAPATEAP  
SPPSTAPPTVGPVPQPQDCPPSTCLNGGTCHLGTRHHLACLCPEGFTGLYCESQMGOQTRPSPTP  
VTPRPPRSLTGIEPVSPSTSLRVGLQRYLQGSSVQLRSRLTYRNLSGPDKRLVTLRLPASIAEY  
TVTQLRPNATYSVCVMPLGPGRVPEGEEACGEAHTPPAVHSNHPVTQAREGNLPLLIAPALAAV  
LLAALAAVGAAVCVRRGRAMAAAQDKGQVPGAGPLELEGVKVPLEPGPKATEGGGEALPSGSE  
CEVPLMGFPGPGLQSPFHAKPYI

**Important features:**

**Signal peptide:**

amino acids 1-23

**Transmembrane domain:**

amino acids 579-599

**EGF-like domain cysteine pattern signature.**

amino acids 430-442

**Leucine zipper pattern.**

amino acids 197-219, 269-291

**N-glycosylation sites.**

amino acids 101-105, 117-121, 273-277, 500-504, 528-532

**Tyrosine kinase phosphorylation sites.**

amino acids 124-131, 337-345

**N-myristoylation sites.**

amino acids 23-29, 27-33, 70-76, 142-148, 187-193, 348-354,  
594-600, 640-646

## FIGURE 17

GCAGCGGCAGGCAGCGGTGGCTGAGTCGTGGCAGAGCGAAGGCACAGCTATGCG  
GGTCGGATAGGGCTGACGCTGCTGTGCGGTGCTGAGCTTGGCTCGCGTCCGG  
ATGAAGAAGGCAGCCAGGATGAATCCTAGATTCAAGACTACTTGACATCAGATGAGTCAGTA  
AAGGACCACTACTGCAGGCAGAGTAGTTGCTGGTCAAATATTCTGATTCAAAGAAATCTGA  
ATTAGAATCCTCTATTCAAGAACAGGAAGACAGCCTCAAGAGCCAAGAGGGGAAAGTGTACAG  
AAGATATCAGCTTCTAGACTCAGAAACAGGACTATGAAGAGCCAAGAAAGTA  
CGGAAACCAGCTTGACGCCATTGAAGGCACAGCACATGGGGAGCCCTGCCACTTCCCTTCT  
TTTCCTAGATAAGGAGTATGATGAATGTACATCAGATGGAGGGAAAGATGGCAGACTGTGGTGT  
CTACAACTATGACTACAAAGCAGATGAAAAGTGGGGCTTTGTGAAACTGAAGAACAGGCTGCT  
AAGAGACGGCAGATGCAGGAAGCAGAAATGATGTATCAAACCTGGAAATGAAAATCCTTAATGGAAG  
CAATAAGAAAAGCCAAAAAGAGAACATATCGGTATCTCCAAAGGCAGCAAGCATGAACCATA  
CCAAAGCCCTGGAGAGAGTGTCAATGCTCTTATTGGTGATTACTGCCACAGAATATCCAG  
GCAGCGAGAGAGATTTGAGAAGCTGACTGAGGAAGGCTCTCCAAAGGGACAGACTGCTCTGG  
CTTCTGTATGCCTCTGGACTTGGTGTAAATTCAAGTCAGGCAAAGGCTTGTATATTACAT  
TTGGAGCTTGGGGCAATCTAATAGCCCACATGGTTTGGTAAAGTAGACTTTAGTGGAAAGGCT  
AATAATATTAACATCAGAAGAATTGTTAGGGTTATAGCGGCCACAACCTTTCAGCTTCATGATC  
CAGATTGCTGTATTAAGACCAAATATTCAAGTGAACCTCCTCAAATTCTGTTAATGGATAT  
AACACATGGAATCTACATGAAATGAAAGTGGTGGAGTCCACAATTTCCTTAAATGATTAG  
TTTGGCTGATTGCCCTAAAAAGAGAGATCTGATAAAATGGCTCTTTAAATTCTGAGTTG  
GAATTGTCAGAATCATTTCATATTAGATTCTAAATTAAAAATTCTTAGTTTCA  
AAATTGTTGAAATGGTGGCTATAGAAAAACACATGAAATATTACAAATATTGCAACATGC  
CCTAAGAATTGTTAAATTCACTGGAGTTATTGTGCTAGGAGCTACTTCTG  
TTTTTACTTTCTGATTGGCTGTCTCCATTATTCTGGTCAATTGTTACTTTCTTGTAAATTGG  
AAGATTAACTCATTAAATAAAATTATGCTAAGATTAAGATTTTTTTTTTTTTTTTTTTTTTT  
AAA

## **FIGURE 18**

MRVRIGLTLLLCAVLLSLASASSDEEGSQDESLSKTTLTSDESVKDHTTAGRVVAGQIFLDSEEESEL  
ESSIQEEEDSLKSQEGERVTEDISFLESPNPNENKDYEPPKKVRKPALTIAEGTAHGEPCCHFPFLFLDK  
EYDECTS DGDREDGRLWCATTYDYKADEKWGFCETEEEAAKRRQMQEAMMYQTGMKILNGSNKSQKR  
EAYRYLQKAASMNHTKALERVSYALLFGDYLQPQNIQAAREMFEKLTEEGSPKGQTALGFLYASGLGVN  
SSQAKALVYYTGFALGGNLIAHMVLVSRL

**Important features:**

**Signal peptide:**

amino acids 1-21

**N-glycosylation sites.**

amino acids 195-199, 217-221, 272-276

**Tyrosine kinase phosphorylation site.**

amino acids 220-228

**N-myristoylation sites.**

amino acids 120-126, 253-259, 268-274, 270-274, 285-291, 289-295

**Glycosaminoglycan attachment site.**

amino acids 267-271

**Microbodies C-terminal targeting signal.**

amino acids 299-303

**Type II fibronectin collagen-binding domain protein.**

amino acids 127-169

**Fructose-bisphosphate aldolase class-II protein.**

amino acids 101-119

## **FIGURE 19**

AATTCAAGTTAACGCCATTCTGCAGTGGAAATTGACTGAACTAGCAAGAGGACACCATTCTT  
GTATTATACAAGAAAGGAGTGTACCTATCACACACAGGGGGAAAAATGCTTTGGGTGCTAGG  
CCTCCTAATCCTCTGGTTCTGTGGACTCGTAAGGAAACTAAAGATTGAAGACATCACTG  
ATAAGTACATTTTATCACTGGATGTGACTCGGGCTTGGAAACTGGCAGCAGAACCTTTGAT  
AAAAAGGGATTCATGTAATCGCTGCCTGCTGACTGAATCAGGATCAACAGCTTAAAGGAGA  
AACCTCAGAGAGACTCGTACTGTGCTCTGGATGTGACCGACCCAGAGAATGTCAAGAGGACTG  
CCCAGTGGGTGAAGAACCAAGTGGGGAGAAAGGTCTCTGGGTCTGATCAATAATGCTGGTGT  
CCCGGCGTGCCTGGCTCCACTGACTGGCTGACACTAGAGGACTACAGAGAACCTATTGAAGTGAA  
CCTGTTGGACTCATCAGTGTGACACTAAATATGCTCCTTGGTCAAGAAAGCTCAAGGGAGAG  
TTATAATGTCTCCAGTGTGGAGGTGCCCTGCAATCGTGGAGGGGCTATACTCCATCCAAA  
TATGCAGTGGAAAGGTTCAATGACAGCTTAAGACGGGACATGAAAGCTTTGGTGTGCACGTCTC  
ATGCATTGAACCAGGATTGTTCAAAACAAACTGGCAGATCCAGTAAAGGTAATTGAAAAAAAC  
TCGCCATTGGGAGCAGCTGTCCTCCAGACATCAAACAATATGGAGAAGGTTACATTGAAAAA  
AGTCTAGACAAACTGAAAGGCAATAAATCCATGTGAAACATGGACCTCTCCGGTGGTAGAGTG  
CATGGACCACGCTCTAACAGTCTCTCCCTAACACTCATTATGCCGCTGGAAAAGATGCCAAA  
TTTCTGGATACCTCTGTCTCACATGCCAGCAGCTTGCAGACTTTTATTGGTAAACAGAAAA  
GCAGAGCTGGCTAACCCCAAGGCAGTGTGACTCAGCTAACCAAAATGTCTCCCTCAGGCTATGA  
AATTGGCCGATTCAGAACACATCTCCTTCAACCCATTCCATTCTGCTCCAACCTGGACT  
CATTTAGATCGTGCCTATTGGATTGCAAAAGGGAGTCCCACCATCGCTGGTGTATCCAGGGT  
CCCTGCTCAAGTTCTTGGAAAGGAGGGCTGGAATGGTACATCACATAGGCAAGTCCCTGCCCT  
GTATTTAGGCTTGCCTGCTGGTGTGATGTAAGGAAATTGAAAGACTTGCCTTCAAAATGA  
TCTTACCGTGGCCTGCCCATGCTTATGGCCCCAGCATTACAGTAACCTGTGAATGTTAAGT  
ATCATCTTATCTAAATATTAAGATAAGTCAACCCAAAAAA  
AAAAAAAAAAAAA

## **FIGURE 20**

MLFWVLGLLILCGFLWTRKGKLKIEDITDKYIFITGCDSGFGNLAARTFDKKGFHVIAACLTESG  
STALKAETSERLRTVLLDVTDPENVKRTAQWVKNQVGEKGLWGLINNAGVPGVIAPTDWLTLEDY  
REPIEVNLFGGLISVTLNMLPLVKKAQGRVINSSVGGRLAIVGGGYTPSKYAVEGFNDSLRRDMK  
AFGVHVSCIEPGLFKTNLADPVKVIEKKLAIWEQLSPDIKQQYGEGYIEKSLDKLKGKNSYVNMD  
LSPVVECMDHALTSLFPKTHYAAAGKDAKIFWIPLSHMPAALQDFLLLKQKAELANPKAV

**Important features of the protein:**

**Signal peptide:**

amino acids 1-17

**Transmembrane domain:**

amino acids 136-152

**N-glycosylation sites.**

amino acids 161-163, 187-190 and 253-256

**Glycosaminoglycan attachment site.**

amino acids 39-42

**N-myristoylation sites.**

amino acids 36-41, 42-47, 108-113, 166-171, 198-203 and 207-212

## **FIGURE 21**

CTGAGGCCGGCGGTAGCATGGAGGGGGAGAGTACGTCGGCGGTGCTCTCGGGCTTGTGCTCGGCG  
CACTCGCTTCCAGCACCTCAACACGGACTCGGACACGGAAGGTTCTTCTGGGAAAGTAAAA  
GGTGAAGCCAAGAACAGCATTACTGATTCCAAATGGATGATGTTGAAGTTGTTATAACAATTGA  
CATTCAAGAAATATATTCCATGCTATCAGCTTTAGCTTTATAATTCTTCAGGCGAAGTAAATG  
AGCAAGCACTGAAGAAAATATTATCAAATGTCAAAAGAATGTGGTAGGTTGGTACAAATTCCGT  
CGTCATTCAAGATCAGATCATGACGTTAGAGAGAGGCTGCTTCACAAAAACTTGCGAGGAGCATTT  
TTCAAAACCAAGACCTTGTCTGCTATTAAACCAAGTATAAAACAGAAAGCTGCTCTACTC  
ATCGACTGGAACATTCTTATATAAACCTCAAAAGGACTTTTACAGGGTACCTTAGTGGTT  
GCCAATCTGGCATGTCGAACAACGGTTATAAAACTGTATCAGGTTCTGTATGTCCACTGG  
TTTAGCCGAGCAGTACAAACACAGCTCTAAATTGGAGAAGATGGATCCTTAAAGGAGG  
TACATAAGATAAAATGAAATGTATGCTTCATTACAAGAGGAATTAAAGAGTATATGCAAAAAGTG  
GAAGACAGTGAACAAGCAGTAGATAAACTAGTAAAGGATGTAACAGATTAAACGAGAAATTGA  
GAAAAGGAGAGGAGCACAGATTCAAGGAGCAAGAGAGAAGAACATCCAAAAGACCCCTCAGGAGA  
ACATTTCCTTGTCAAGGCACTACGGACCTTTTCAAAATTCTGAATTCTTCATTCACTGTGTT  
ATGTCTTAAAAAATAGACATGTTCTAAAGTAGCTGTAACATAACACCACATCTCGATGTAGT  
AGACAATCTGACCTTAATGGAGAACACACTGACATTCTGAAGCTAGTCCAGCTAGTACACCAC  
AAATCATTAAAGCATAAAGCCTTAGACTTAGATGACAGATGGCAATTCAAGAGATCTGGTTGTTA  
GATACACAAGACAAACGATCTAAAGCAAATACTGGTAGTAGTAACCAAGATAAAGCATCCAAAAT  
GAGCAGCCCAGAAACAGATGAAGAAATTGAAAAGATGAAGGGTTTGGTGAATATTACGGTCTC  
CTACATTTGATCTTTAACCTTACAAGGAGATTTTATTGGCTGATGGTAAAGCCTAACAC  
ATTCTATTGTTTACTATGAGCTACTGAGCTACTGAGCTACTGAGCTACTGAGCTACTGAGCTACT  
TGTTGAGCTACTGAGCTACTGAGCTACTGAGCTACTGAGCTACTGAGCTACTGAGCTACT  
GATGCTTTATTCCAAACCTTTTACCTTCACTAAGTTGAGCTACTGAGCTACTGAGCTACT  
ACACATTCTTAAAGCAGGAGCTACTGAGCTACTGAGCTACTGAGCTACTGAGCTACT  
TAGGGAAGACAAGTCAGGAGGATTGAGCTAGGAGTTAGAGACCAAGCCTGGCAACGTATT  
GAGACCATGCTATTAAAAAATGAAAAGCAAGAATAGCCTTATTTCAAAATATGGAAA  
GAAATTATATGAAAATTATCTGAGTCATTAAATTCTCCTTAAGTGTAACTTTTAAAGTA  
CATTATGGCTAGAGTTGCCAGATAAAATGCTGGATATCATGCAATAATTGCAAAACATCATCT  
AAAATTAAAAAAAAAAAAAAAAAAAAA

## **FIGURE 22**

MEGESTSAVLSGFVLGALAFQHLNTSDTEGFLLGEVKGEAKNSITDSQMDDVEVVYTIDIQKYI  
PCYQLFSFYNSSGEVNEQALKKILSNVKKNVVGWYKFRRHSDQIMTFRERLLHKNLQEHFSNQDL  
VFLLLTPSIITESCSTHRLEHSLYKPQKGLFHRVPLVVANLGMSEQLGYKTVSGSCMSTGFSRAV  
QTHSSKFFEDGSLKEVHKINEMYASLQEELKSICKVEDSEQAVDKLVKDVNRLKREIEKRRGA  
QIQAAREKNIQKDPQENIFLCQALRTFFPNSEFLHSCVMSLKNRHVSKSSCNYNHLDVVDNLTL  
MVEHTDipeASPASTPQIIKHKALDLDDRQFKRSRLLDTQDKRSKANTGSSNQDKASKMSSPET  
DEEIEKMKGFGEYSRSPTF

**Important features:**

**Signal peptide:**

amino acids 1-19

**N-glycosylation sites.**

amino acids 75-79, 322-326

**N-myristoylation site.**

amino acids 184-154

**Growth factor and cytokines receptors family.**

amino acids 134-150

## **FIGURE 23**

GGCACAGCCGCGCGGGGGAGGGCAGAGTCAGCCGAGCCGAGTCAGCCGAGCCGACAGCGGACCGAGCGCAGGGCAGCCAA  
GCAGCGCGCAGCGAACGCCCGCGCCGCCACACCCCTGCGGTCCCGCGGCCTGCCACCCCTCCCTCCCTCCCC  
GCGTCCCCGCGCTCGCCGCCAGTCAGCTTGCCTGGGGTCAGCTGCCCGCGAAACCCCGAGGTACCCAGCCCGCGCCTCT  
GCTTCCCTGGCCGCGCGCCGCCACGCCCTCCTCTCCCGCTGCCGTCCACCGGGGACCGTTGCC  
CGCAGGGCCCAGCTACTTTGCCCGCGCTCTCCGCTGCCCTCTCCACCAACTCCAACCTCCCTCCCC  
TCCAGCTCCACTCGCTAGTCCCCGACTCCGCCAGCCCTGCCGTAGCGCCGCTCCCGTCCGGTCCAAA  
GGTGGGAACCGCTCCGCCCGGCCGACCAATGGCACGGTTGGCTTGCACCCGCGCTCTGCACCTGGCAGTGC  
AGCGCCGCGCTGGCTGCCGAGCTAACGCTGAAAAGTTGCTCGAAGTGCAGCTTTACGTGTCAAAGGCTC  
AACAGAACGATGCCCTCCACGAGATCAACGGTATCATTGAAGATCTGCCCCAGGGTCTACCTGCTGCT  
CAAGAGATGGAGGAGAAGTACAGCTGCAAAGTAAGATGATTCAAAGTGTGGTCAGCGAACAGTGAATCATTG  
CAAGCTGCTTGTCTCACGTTACAAGAAGTTGATGAATTCTCAAAGAACTACTTGAAAATGCAGAGAAATCCCTG  
AATGATATGTTGTGAAGACATATGGCATTATACATGCAAATTCTGAGCTATTAAAGATCTCTCGTAGAGTTG  
AAACGTTACTACGTGGGGAAATGTAACCTGGAAAGAAATGCTAAATGACTTCTGGGCTCGCCCTGGAGCGGATG  
TTCCGCTGGTGAACCTCCAGTACCACTTACAGATGAGTATCTGGATGTGTGAGCAAGTATACGGAGCAGCTGAAG  
CCCTTGGAGATGCTCCCGCAAATTGAAGTCCAGGTTACTGTCGTTTGATGAGCCCTACTTCGCTCAAGGC  
TTAGCGGGTGGGGAGATGTCGTGAGCAAGGTCTCCGTGGTAACCCACAGCCAGTGTACCCATGCCCTGTTGAAG  
ATGATCTACTGCTCCCACTGCCGGGTCTCGTGACTGTGAAGCCATGTTACAACACTGCTCAAACATCATGAGAGGC  
TGGTGGCCAACCAAGGGATCTGATTTGAATGGAACATTTCAGATGCTATGCTGATGGTGGAGAGAGGCTA  
GAGGGTCTTCAACATTGAATCGGTATGGATCCCATCGATGTGAAGATTCTGATGCTATTATGAACATGCGAGGAT  
AATAGTGTCAAGTGTCTCAGAAGGTTTCCAGGGATGTTGACCCCTCCAGCTGGAGAATTTCG  
TCCATCTGAAAGTGCCTCAGTGCCTCGACACCACATCACCAGGAACGCCAACACAGCAGCTGGCACT  
AGTTGGACCACTGGTTACTGATGTCAGGAGAACTGAAACAGGCAAGAAATTCTGGCCTCCCTCCGACCAAC  
GTTGCAACGATGAGAGGATGGCTGAGGAACCGCAATGAGGATGACTGTTGAATGGAAAGGGCAAAAGCAGGTAC  
CTGTTGCACTGACAGGAAATGGATTAGCAACCAGGGCAACAAACCCAGAGGTCCAGGTTGACACCAGCAAACAGAC  
ATACTGATCTCGTCAAATCATGCCCTTCGAGTGTGACCAAGATGAAGAATGCAACATGGAACAGCTG  
GACTTCTTGATATCAGTGTGAAAGTAGTGGAGAAGGAAGTGGAGTGGCTGTGAGTATCAGCAGTGCCTTCAGAG  
TTTGACTACAATGCCACTGACCATGCTGGAGAGTCCCAATGAGAAAGCCGACAGTGTGCTGGTCCCTGGGGCA  
CAGGCCACCCACTGCTCTGCACTTGTGTTGGTATGCAAGAGAGTGGAGAATCTCAAACACTGAG  
AAAAAGTGTTCATCAAAAGTAAAGGCAACAGTTATCACTTTCTACCATCTAGTGACTTGCTTTAAATGAA  
TGGACAACAAATGACAGTTTACTATGTTGCACTGGTTAAGAAGTGTGACTTGTGTTCTCATTCAGTTGG  
AGGAAAAGGGACTGTGCAATTGAGTTGGTCTGCTCCCCAACCATGTTAAACGTTGGCTAACAGTGTAGGTACAGAA  
CTATAGTTAGTTGTGCAATTGATTTTACTCTATTATGTTGTTATGTTTTCTCATTCGTTGTTGG  
TTTTTTCCAACTGTGATCTCGCCCTGTTCTACAAGCAAACCAAGGGTCCCTTGGCACGTAACATGTACGTT  
TCTGAAATATTAATAGCTGTACAGAACAGGTTTATTTATCATGTTATCTTAAAGAAAAAGCCAAAAAGC

## **FIGURE 24**

MARFGLPALLCTLAVLSAALLAELKS KSCSEVRRLYVSKGF N KNDAPLHEINGDHLKICPQGST  
CCSQEME EKYS LQS KDD FKS VVSE QCNH LQAVFASRYKKFDEFFKELLENAEKSLNDMFVKT YGH  
LYMQNSEL FKDLF VELKRYVVG NVNLE EMLNDFWARLLERMFR LVNSQYHFTDEYLECVSKY TE  
QLKPFGDV PRKLKLQVTRAFVAARTFAQGLAVAGDV VSKV SVNPTA QCTHALLKMIYCSHCRGL  
VTVKPCNYCSNIMRGCLANQGDLDFEWNNFIDAMLMVAERLEGP FNIESVMDP IDVKISDAIMN  
MQD NSVQVSQKV FQGC GPPKPLPAGRISRSI SEAFSARFRPHHPEERPTTAAGTSLDR LVT DVK  
EKLKQAKKF WSSLPSNV CNDERMAAGNGN EDDC WNGKGK SRYL FAVTGNGLANQGN NPEVQV DTS  
KPDILILRQIMALRVMTSKMKNAYNGNDV DFFDISDESSGEGSGSGCEYQQCPSEFDY NATDHAG  
KSANEKADSAGV RPGAQAYLLTVFCILFLVMQREWR

**Important features:**

**Signal peptide:**

amino acids 1-22

**ATP/GTP-binding site motif A (P-loop).**

amino acids 515-524

**N-glycosylation site.**

amino acids 514-518

**Glycosaminoglycan attachment sites.**

amino acids 494-498, 498-502

**N-myristoylation sites.**

amino acids 63-69, 224-230, 276-282, 438-444, 497-503, 531-537

**Glypicans proteins.**

amino acids 54-75, 105-157, 238-280, 309-346, 423-460, 468-506

## **FIGURE 25**

CTCGCCCTCAAATGGAACGCTGGCTGGACTAAAGCATAGACCACCAGGCTGAGTATCCTGAC  
CTGAGTCATCCCCAGGGATCAGGGCCTCCAGCAGGGAACCTCATTATATTCTTCAGCAACT  
TACAGCTGCACCGACAGTTGCCGAAAGTTCTAATCTTCCCTCCTGTTGCTGCCACTAA  
TGCTGATGTCCATGGTCTCTAGCAGCCTGAATCCAGGGTCGCCAGAGGCCACAGGGACCAGGC  
CAGGCTCTAGGAGATGGCTCCAGGAAGGCGCCAAGAACATGTGAGTGCAAAGATTGGTCCTGAG  
AGCCCCGAGAAGAAAATTATGACAGTGTCTGGGCTGCCAAAGAACAGCAGTGCCCTGTGATCATT  
TCAAGGGCAATGTGAAGAAAACAAGACACCAAAAGGCACCCACAGAACGCCAAACAAGCATTCCAGA  
GCCTGCCAGCAATTCTCAAACAATGTCAGCTAAGAACGCTTGTCTGCCCTTGTAGGAGCTCTG  
AGCGCCCACTCTCCAATTAAACATTCTCAGCCAAGAACAGTGTGAGCACACCTACCAAGACACTC  
TTCTCTCCCACCTCACTCTCCACTGTACCCACCCCTAAATCATCCAGTGTCTCTCGTCAGTCTTAGCCT  
TGTTTTCAAGATCATTGTTGTTGCTCTCTAGTGTCTCTCTCGTCAGTCTTAGCCT  
GTGCCCTCCCTTACCCAGGCTTAGGCTTAATTACCTGAAAGATTCCAGGAAACTGTAGCTTCCT  
AGCTAGTGTCAATTAAACCTTAAATGCAATCAGGAAAGTAGCAAACAGAACAGTCAATAAATATTTT  
AAATGTCAAAAAAAAAAAAAAAA

## **FIGURE 26**

MKVLISSLLLLPLMLMSMVSSSLNPVARGHDRGQASRRWLQEGGQECECKDWFLRAPRRKFM  
TVSGLPKKKQCPDCDFKGNVKKTRHQRHHRKPNKHSRACQQFLKQCQLRSFALPL

**Important features:**

**Signal peptide:**

amino acids 1-22

**N-myristoylation sites.**

amino acids 27-33, 46-52

## **FIGURE 27**

GGACGCCAGCGCCTGCAGAGGCTGAGCAGGGAAAAGCCAGTGCCCCAGCGGAAGCACAGCTCAG  
AGCTGGCTGCCATGGACATCCTGGTCCCCTGCAGCTGCTGGTCTGCTCTTACCCGCC  
CCTGCACCTCATGGCTCTGCTGGCTGCTGGCAGCCCCGTGCAAAAGCTACTTCCCCTACCTGA  
TGGCGTGTGACTCCAAGAGCAACCGCAAGATGGAGAGCAAGAACGGGAGCTTCAGCCAG  
ATAAAGGGGCTTACAGGAGCCTCCGGAAAGTGGCCCTACTGGAGCTGGCTGCCAACCGGAGC  
CAACTTCAGTTCTACCCACCGGGCTGCAGGGTCACCTGCCTAGACCCAAATCCCCACTTGAGA  
AGTTCCGTACAAAGAGCATGGCTGAGAACAGGCACCTCAATATGAGCGGTTGTGGCTCCT  
GGAGAGGACATGAGACAGCTGGCTGATGGCTCCATGGATGTGGTGTGCACCTGGTGTG  
CTCTGTGCAGAGCCAAGGAAGGTCTGCAGGAGGTCCGGAGAGTACTGAGACCCGGAGGTGTG  
TCTTTTCTGGGAGCATGTGGCAGAACCATATGGAAGCTGGCCTTCATGTGGCAGCAAGTTTC  
GAGCCCACCTGGAAACACATTGGGATGGCTGCCTCACAGAGAGACCTGGAAGGATCTTGA  
GAACGCCAGTTCTCCGAAATCAAATGGAACGACAGCCCCCTCCCTGAAGTGGCTACCTGTTG  
GGCCCCACATCATGGAAAGGCTGCAAACAATTTCCAAGCTCCAAGGCACACTATTGCTCC  
TTCCCCAGCCTCAAATTAGAACAGCCACCCACCAGCCTATCTATCTTCACTGAGAGGGACTA  
GCAGAACATGAGAGAACATTGATGTACCACTACTAGTCCCTCTCCTCCAAACCTGCCCAGGG  
AATCTCTAACTCAATCCCGCCTCGACAGTAAAAAGCTCTACTTCTACGCTGACCCAGGGAGG  
AAACACTAGGACCCCTGTTGATCCTCACTGCAAGTTCTGGACTAGTCTCCAAACGTTGCTC  
CCAATGTTGTCCTTCCCTCGTTCCATGGTAAAGCTCCTCTCGCTTCCCTGAGGCTACAC  
CCATGCGTCTCTAGGAACCTGGTCACAAAAGTCATGGTGCCTGCATCCGTCCAAGCCCCCTGAC  
CCTCTCTCCCCACTACCACCTTCTGAGCTGGGGCACCAGGGAGAATCAGAGATGCTGGG  
ATGCCAGAGCAAGACTCAAAGAGGCAAGAGGTTTGTCTCAAATTTTTAATAAAATAGACGAA  
ACCACG

## **FIGURE 28**

MDILVPLLQLLVLLTLPLHLMALLGCWQPLCKSYFPYILMAVLTPKSNRKMESKKRELFSQIKGL  
TGASGKVALLELGCCTGANFQFYPPGCRVTCLDPNPHFEKFLTKSMAENRHLQYERFVVAPGEDM  
RQLADGSMVVVCTLVLCVQSPRKVLQEVRRVLRPGVLFFWEHVAEPYGSWAFMWQQVFEPTW  
KHIGDGCLTRETWKDLENAQFSEIQMERQPPPLKWLPGPHIMGKAVKQSFPSSKALICSFPSL  
QLEQATHQPIYLPLRGT

**Important features:**

**Signal peptide:**

amino acids 1-23

**Leucine zipper pattern.**

amino acids 10-32

**N-myristoylation sites.**

amino acids 64-70, 78-84, 80-86, 91-97, 201-207

## **FIGURE 29**

CAATTTGCCTATCCACCTCCCCAAGCCCCTTACCTATGCTGCTGCTAACGCTGCTGCTGCT  
GCTGCTGCTAAAGGCTCATGCTGGAGTGGGACTGGTCGGGCCAGAAAGTCTCTCTG  
CCACTGACGCCCCATCAGGGATTGGGCCTCTTCCCCCTCCTTCTGTGTCTCCTGCCTCAT  
CGGCCTGCCATGACCTGCAGCCAAGCCCAGCCCCGTGGGAAGGGGAGAAAGTGGGGATGGCTA  
AGAAAGCTGGGAGATAGGAACAGAACAGAGGGTAGTGGGTGGCTAGGGGGCTGCCTTATTAAA  
GTGGTTGTTATGATTCTTATACTAATTATAACAAAGATATTAAGGCCCTGTTCATTAAGAAATT  
GTTCCCTTCCCTGTGTTCAATGTTGTAAAGATTGTCTGTGTAAATATGTCTTATAATAAAC  
AGTTAAAAGCTGAAAAAAAAAAAAAAAAAAAAAAAAAAAAAA

## **FIGURE 30**

MLLLTLLLLLKGSCLEWGLVGAQKVSSATDAPIRDWAFFPPSFLCLLPHRPAMTCSQAQPRG  
EGEKVGDG

**Important features:**

**Signal peptide:**

amino acids 1-15

**Growth factor and cytokines receptors family:**

amino acids 3-18

## **FIGURE 31**

GTGTTGAATTCCCTTCAACTATAACCCACAGTCCAAAAGCAGACTCACTGTGTCCCAGGCTACCAGTT  
CCTCCAAGCAAGTCATTTCCCTTATTAAACCGATGTGTCCCTCAAACACCTGAGTGCTACTCCCT  
ATTTGCATCTGTTGATAAATGATGTTGACACCCCTCACCAGAATTCTAAGTGAATCATGTCGG  
GAAGAGATAACAATCCTGGCCTGTGTATCCTCGCATTAGCCTGCTTGCCATGATGTTAC  
TTCAGAGATTCACTACCACCCCTCTGGTCACATTTCATTCATTGGTTATTTGGGATTGTTGTT  
TGTCTGCGGTGTTTATGGTGCCTGTATTATGACTATAACCAACGACCTCAGCATAGAATTGGACA  
CAGAAAAGGAAAATATGAAGTGCCTGTGGGTTTGCATCGTATCCACAGGCATCACGGCAGTG  
CTGCTCGTCTGATTTGTTCTCAGAAAAGAGAATAAAATTGACAGTTGAGCTTTCCAAATCAC  
AAATAAAGCCATCAGCAGTGCTCCCTTCCTGCTGTTCCAGCCACTGTGGACATTGCCATCCTCA  
TTTTCTCTGGGTCTCTGGGGCTGTGCTGCTGAGCCTGGGAACTGCAGGAGCTGCCAGGTT  
ATGGAAGGCGGCCAAGTGAATATAAGCCCTTCGGGCATTGGTACATGTGGTGTACCATTT  
AATTGGCCTCATCTGGACTAGTGAATTCATCCTTGCCTGCCAGCAAATGACTATAGCTGGGCAG  
TGGTTACTGTTATTCACAGAAGTAAAAATGATCCTCCTGATCATCCCATCCTTCGTCTCTC  
TCCATTCTCTTCTTCTACCATCAAGGAACCGTTGTGAAAGGGTCAATTAAATCTCTGTGGTGAG  
GATTCCGAGAATCATTGTCATGTACATGCAAAACGCACTGAAAGAACAGCAGCATGGTGCATTG  
CCAGGTACCTGTCGATGCTACTGCTGTTCTGGTGTCTGACAAATACCTGCTCCATCTC  
AACCGAGAATGCATATACTACAACGTCTATTAAATGGGACAGATTCGTACATCAGAAAAGATGC  
ATTCAAAATCTTGTCCAAGAAACTCAAGTCACCTTACATCTATTAAACTGCTTTGGAGACTTCATAA  
TTTTCTAGGAAAGGTGTTAGTGGTGTGTTCACTGTTGGAGGACTCATGGCTTTAACTAC  
AATCGGGCATTCCAGGTGTGGCAGTCAGAAAAGCCCTACTTATGGATCAAGAATTCTGAGTTCGTA  
CCATAGTTTTATCTGTGTTGAAACTGTGCTGGATGCACCTTCCTGTGTTGCTGTTGATC  
TGGAAACAAATGATGGATCGTCAGAAAAGCCCTACTTATGGATCAAGAATTCTGAGTTCGTA  
AAAAGGAGCAACAAATTAAACAATGCAAGGGCACAGCAGGACAAGCAGTCATTAAGGAATGAGGA  
GGGAACAGAACTCCAGGCCATTGTGAGATAGATACCCATTAGGTATCTGTACCTGGAAAACATT  
TCCTTCTAAGAGGCCATTACAGAATAGAAGATGAGACCACTAGAGAAAAGTTAGTGAATTTTT  
TTAAAAGACCTAATAAACCCATTCTCCTCAAA

## **FIGURE 32**

MSGRTDTILGLCILALALSIAMMFTFRFITLLVHIFISLVLGLLFVCGVLWWLYDYTNDSLIE  
LDTERENMKCVLGFAIVSTGITAVLLVLIFVLRKRIKLTVELFQITNKAISAPFLLFQPLWTFA  
ILIFFWVLWVAVLLSLGTAGAAQVMEGGQVEYKPLSGIRYMWSYHLIGLIWTSEFILACQQMTIA  
GAVVTCYFNRSKNDPPDHPILSSLSILFFYHQGTVVKGSFLISVVRIPRIIVMYMQNALKEQQHG  
ALSRYILFRCCYCCFWCLDKYLLHLNQNAYTTAINGTDFCTSAKDAFKILSKNSSHFTSINCFGD  
IIIFLGKVLVVCFTVFGGLMAFNYNRAFQVWAVPLLLVAFFAYLVAHSFLSVFETVLDALFLCFA  
VDLETNDGSSEKPYFMDQEFLSFVKRSNKLNNARAQQDKHSLRNEEGTELQAIVR

**Important features:**

**Signal peptide:**

amino acids 1-20

**Putative transmembrane domains:**

amino acids 35-54, 75-97, 126-146, 185-204, 333-350, 352-371

**N-glycosylation sites.**

amino acids 204-208, 295-299, 313-317

**N-myristoylation sites.**

amino acids 147-153, 178-184, 196-202, 296-275, 342-348

## **FIGURE 33**

GTTCGATTAGCTCCTCTGAGAAGAAGAGAAAAGGTTCTGGACCTCTCCCTGTTCTCCTAGA  
ATAATTGTATGGGATTTGTGATGCAGGAAGCTAACAGGCTAACAGGGTGTCAATTCTGTGTGGT  
GAAAATTTGAAAAAAATTCGCTTCTCAAAACAAGGGTGTCAATTCTGTGATATTATGAGGAC  
TGTTGTCTCACTATGAGGCATCTGTATTGAAATGTCCTGTTGCTGGTGAATGGAGTAC  
ATTCAAACAAAGAACGGCAAAGAAGATTAAGGGCCAAGTCACTGTGCCTCAGATCAACTGC  
GATGTCAAAGGGAAAAGATCATCGATCCTGAGTCATGTAAATGTCAGCAGGATGCCAAGA  
CCCCAAATACCATGTTATGGCACTGACGTATGCATCTACTCCAGTGTGTGGCGTGCG  
TACACAGTGGTGTGCTTGATAATTCAAGGAGGAAAATATTGTCGGAAAGGTTGCTGGACAGTCT  
GGTTACAAAGGGAGTTATTCCAACGGTGTCCAATCGTTATCCCTACCACGATGGAGAGAACTCTT  
TATCGTCTTAGAAAGTAAACCCAAAAGGGTGTAACTTACCCATCAGCTTACATACTCATCAT  
CGAAAAGTCCAGTCCCAGCAGGTGAGACCCAAAAGCTATCAGAGGCCACCTATTCCAGGG  
ACAACAGCAGCCGGTCACTCTGATGCAGCTCTGGCTGTCACTGTAGCTGTGGCCACCCCCAC  
CACCTTGCCAAGGCCATCCCCCTCTGCTGCTCTACCCACAGCATCCCCAGACCAATCAGTGG  
GCCACAGGAGCCAGGGAGATGGATCTCTGGTCCACTGCCACCTACACAAGCAGCCTAACAGGCC  
AGAGCTGATCCAGGTATCCAAAAGGCAAGATCCTCAGGAGCTGCCCTCCAGAAACCTGTTGGAGC  
GGATGTCAGCCTGGGACTTGTCCAAAAGAAGAATTGAGCACACAGTCTTGAGGCCAGTATCCC  
TGGGAGATCCAAACTGCAAATTGACTTGTGTTTAATTGATGGGAGCACCAGCATTGGCAA  
CGGCGATTCCGAATCCAGAAGCAGCTCTGGTGTGATGTTGCCAAGCTCTTGACATTGGCCCTGC  
CGGTCCACTGATGGGTGTTGTCAGTATGGAGACAAACCTGCTACTCACTTTAACCTCAAGACAC  
ACACGAATTCTCGAGATCTGAAGACAGCCATAGAGAAAATTACTCAGAGAGGAGGACTTCTAAT  
GTAGGTCGGGCATCTCTTGTGACCAAGAACCTTCTTCCAAAGCCAATGGAAACAGAACGG  
GGCTCCAATGTGGTGGTGTGATGGTGGATGGCTGGCCACGGACAAAGTGGAGGAGGCTCAA  
GACTTGCAGAGAGTCAGGAATCAACATTTCATCACCATTGAAGGTGCTGCTGAAAATGAG  
AAGCAGTATGTGGTGGAGCCAACTTTGCAACAAACAAGGGCGTGTGAGAACAAACGGCTTCACTC  
GCTCCACGTGCAGAGCTGGTTGGCCTCCAAAGACCCCTGCAGCCTCTGGTGAAGCGGGCTGCG  
ACACTGACCGCCTGCCCTGCAGCAAGACCTGCTGAACCTGGCTGACATTGGCTCGTCACTGAC  
GGCTCCACGAGTGTGGGGACGGCAACTTCCGACCCGTCACGGTCCAGTTGTGACCAACCTCACCAA  
AGAGTTGAGATTTCCGACACGGGACACGCCATCGGGCCGTGCAAGTACACCTACGAACAGCGGC  
TGGAGTTGGGTTGCAAGTACAGCAGCAAGGGGCTGCCATCAACTTCCGCTGGAGCAGCTCTTCAAGAA  
TACTGGAGTGGTGGCACCAGCACGGGGCTGCCATCAACTTCCGCTGGAGCAGCTCTTCAAGAA  
GTCCAAGCCAAACAGAGGAAGTTAATGATCCTCATCACCAGCAGGGAGGTCTACGACGACGTCC  
GGATCCACGCCATGGCTGCCATCTGAAGGGAGTGTACACCTATGCGATAGGCGTTGCCTGGCT  
GCCCAAGAGGAGCTAGAAGTCACTGGCAACTCAGCAGCAACGGGCTGCCATCAAGGGTGGC  
GTTTGACAAACCTCCATCAGTATGTCCCCAGGATCATCCAGAACATTGTACAGAGTTCAACTCAC  
AGCCTCGGAACTGATTCAAGCAGCAGGAGCACCAGCAAGTGTGCTTTACTAACTGACGTGTT  
GGACCAACCCACCGCTTAATGGGGCACGCACGGTGATCAAGTCTGGCAGGGCATGGAGAAC  
AAATGTCTGTTATTATTCTTGCCATCATGCTTTCTATATTCCAAAACATTGGAGTTACAAAGA  
TGATCACAACAGTATAGAATGAGCAAAAGGCTACATCATGTTGAGGGTGTGGAGATTTACAT  
TTTGACAAATTGTTCAAATAATGTCGGAATACAGTGTGAGCCCTACGACAGGCTTACGTAG  
AGCTTTGTGAGATTTAAGTTGTTATTCTGATTTGAACTCTGTAACCCCTACGCAAGTTCACT  
TTTGTCATGACAATGTAGGAATTGCTGAATTAAATGTTAGAAGGATGAAAATAAAAAA  
AAA  
AAAAAAAAAAAAAAAAAAAAAAAAAAAAA

## **FIGURE 34**

MRTVVLTMKASVIEMFLVLLVTGVHSNKETAKKIKRPKFTVPQINCDVKAGKIIDPEFIVKCPAG  
CQDPKYHVGTDVYASYSSVCGAAVHSGVLDNSGGKILVRKVAGQSGYKGSYSNGVQSLSLPRWR  
ESFIVLESKPKKGVTYPSALTYSSSKPAAQAGETTKAYQRPIPQTTAQPVTLMQLLAVTVAVA  
TPTTLPRPSPSAASSTTSIPRQSVGHRQEMDLWSTATYTSSQNRPRADPGIQRQDPSGAAFQKP  
VGADVSLGLVPKEELSTQSLEPVSLGDPNCKIDLSFLIDGSTSIGKRRFRIQKQLLADVAQALDI  
GPAGPLMGVVQYGDNPATHFNLKHTNSRDLKTAIEKITQRGGLSNVGRAISFVTKNFFSKANG  
RSGAPN VVVVMV DGWPTDKV EEA SRLA RES GIN IFFITIE GAA ENEK QYV VEPN FANK A V CRT NG  
FYSLHVQSWFGLHKT LQPLVKRVC DTLAC SKT CLNSA DGF VIDG SSSV GTGN FRTV LQF VTN  
LTKEFEI S DTDTRIGAVQYTYEQRLEFGFDKYSSKPDILNAIKR VGYW SGGT STGA A INF ALE QL  
FKKSKPNKRKLMILITDGRSYDDVRI PAMA AHLKG VITYAIGVAWA A QEE LEVI A THPARDHSFF  
VDEF DNLHQYVPRIQNICTEFNSQPRN

**Important features:**

**Signal peptide:**

amino acids 1-26

**Transmembrane domain:**

amino acids 181-200

**N-glycosylation sites.**

amino acids 390-394, 520-524

**N-myristoylation sites.**

amino acids 23-29, 93-99, 115-121, 262-268, 367-373, 389-395,  
431-437, 466-472, 509-515, 570-576, 571-577, 575-581, 627-633

**Amidation site.**

amino acids 304-308

## **FIGURE 35**

CCGAGCACAGGAGATTGCCTGCCTTAGGAGGTGGCTGCCTGTGGAAAAGCTATCAAGGAAGAAATTGC  
CAAACCATGCTTTTTCTGTTCAAGAGTAGTCACAACAGATCTGAGTGTGTTAATTAAGCATGGAAT  
ACAGAAAACAACAAAAAACTTAAGCTTAATTCATCTGGAAATTCCACAGTTCTTAGCTCCCTGGACCC  
GGTTGACCTGTTGGCTTCCCGCTGGCTGCTCTACGTTGGTCTCCGACTACTCACCCCGAGTGTAA  
AAGAACCTCGGCTCGCGTCTGAGCTGCTGGATGGCCTCGCTCTGGACTGCTCCGAGTGTAA  
GGATGTCACTGAGATCCCTAAATGGAGCCTCCTGCTGCTGCACTCCTGAGTTCTTGATGTGGTAC  
CTCAGCCTCCCCACTACAATGTGATAGAACCGGTAACTGGATGTACTCTATGAGTATGAGCCGATTAA  
CAGACAAAGACTTCACCTCACACTCGAGAGCATTCAAACGCTCTCATCAAATCCATTCTGGTCATT  
TGGTGACCTCCCACCCCTCAGATGTGAAAGCCAGGCAAGGCTTACTTGGGGTGAAGAAAAGTCT  
TGGTGGGGATATGAGGTTCTACATTTCTTATTAGGCCAAGAGGCTGAAAGGAAGACAAAATGTTGGC  
ATTGTCCTTAGGGATGAACACCTCTTATGGGACATAATCCGACAAGATTTTAGACACATATAATA  
ACCTGACCTGAAAACCATTATGGCATTCAAGGGTAACTGAGTTTGCCTTAACTGCAAGTACGTAATG  
AAGACAGACACTGATGTTTCATCAAACTGGCAATTAGTGAAGTATCTTAAACCTAAACCACTCAGA  
GAAGTTTACAGGTTATCCTAATTGATAATTATTCTATAGAGGTTACCAAAAACCCATATT  
CTTACCAAGGAGTATCCTTCAAGGTGTTCCCTCATACTGCAGTGGGTTAGTATAATGTCAGAGAT  
TTGGTGCCAAAGGATCTATGAAATGATGGGTCACGTAACCTCAAGTTGAAGATGTTATGTCGGGAT  
CTGTTGAATTATTAAAAGTGAACATTCAATTCCAGAAGACACAATTCTTCTTATAGAAT  
ATTGGATGTCTGCAACTGAGACGTGTGATTGCGAGCCATGGTTTCTTCAAGGAGATCATCACTTT  
TGGCAGGTCATGCTAAGGAACACCATGCCATTATTAAACTCACATTCTACAAAAGCCTAGAAGGACAG  
GATACCTGTGAAAGTGTAAATAAGTAGGACTGTGGAAAATTCTAGGGAGGTCACTGTCGTGGCTT  
ACACTGAAACTCATGAAAACCCAGACTGGAGACTGGAGGGTTACACTTGTGATTTATTAGTCAGG  
CCCTTCAAAGATGATATGTGGAGGAATTAAATAAGGAATTGGAGGTTTGCTAAAGAAATTAAATAGG  
ACCAAACAATTGGACATGTCACTGTAGACTAGAATTCTTAAAGGTGTTACTGAGTTATAAGCTCA  
CTAGGCTGAAAAACAAACATGTAGAGTTTATTGAAACAATGTAGTCAGTCACTGAAGGTTTGCTGTA  
TATCTTATGTGGATTACCAATTAAAAATATGTAGTTCTGTGTCAAAAAACTTCACTGAAGTTATA  
CTGAACAAAATTTCACCTGTTTGGTCATTATAAAAGTACTTCAGTCAAGATGTCAGTATTTCACAGTTATT  
ATTATTTAAAATTACTTCACCTTGTGTTTAAATGTTTGACGATTCAACATAAGATAAAAAGGATAG  
TGAATCATTCTTACATGCAAACATTCCAGTTACTTAACGTGATCAGTTATTATTGATAACACTCCA  
TTAATGTAAGTCATAGGTCAATTGCAATATCAGTAATCTTGGACTTGTAAATTTACTGTGGT  
AATATAGAGAAGAATTAAAGCAAGAAAATCTGAAAAA

## **FIGURE 36**

MASALWTVLPSRMSLRSLKWSLLLLSLLSFFVMWYLSLPHYNVIERVNWMYFYEYEPIYRQDFHF  
TLREHSNCSSHQNPFLVILVTSHPSDVKARQAIRVTWGEKKSSWWGYEVLTFFLLGQEAEKEDKMLA  
LSLEDEHLLYGDIIHQDFLDTYNNLTAKTIMAFRWVTEFCPNAKYVMKTDVFINITGNLVKYLL  
NLNHSEKFFTGYPLIDNYSYRGFYQKTHISYQEYPFKVFPPYCSGLGYIMSRDLVPRIYEMMGHV  
KPIKFEDVYVGICLNLLKVNIHIPEDTNLFFLYRIHLDVCQLRRVIAAHGFSSKEIITFWQVMLR  
NTTCHY

**Important features:**

**Type II transmembrane domain:**

amino acids 20-39

**N-glycosylation sites.**

amino acids 72-76, 154-158, 198-202, 212-216, 326-330

**Glycosaminoglycan attachment site.**

amino acids 239-243

**Ly-6 / u-PAR domain proteins.**

amino acids 23-37

**N-myristoylation site.**

amino acids 271-277

## **FIGURE 37**

CGCTCGGGCACCGCCGGCAAGGAGGAGCTGGGTGCTGGACGCAGTTGGGCTCACTTCTCAGCTCCTTCATC  
TCGTCCTGCCAAGAGAGTACACAGTCATTAATGAAGCTGCCCTGGACAGACTGGAATATCATGTCGGAGTGTG  
AATATGATCAGATTGAGTCGTCTCCCCGGAAAGAGGGAAAGTGTGGGTATACCATCCCTTGCTGCAGGAATGAGGAGAA  
TGAGTGTGACTCCCTGCCATCCACCCAGGTTGACCATCTTGAAACTGCAAGAGCTGCCGAAATGGCTATGGGGGT  
ACCTTGGATGACTCTATGTGAAGGGGTTCTACTGTGCAGAGTGCAGCAGGGCTGGTACGGAGGAGACTGCATGCGATGTG  
GCCAGGGTCTGCGAGCCCAAAGGGTCAGATTTGGAAAGCTATCCCTAAATGCTACTGTGAATGGACCATTCATGC  
TAAACCTGGGTTGTGATCCAACTAAGATTGTCATGTTGAGTGTGGAGTTGACTACATGTGCCAGTATGACTATGTTGAG  
GTTCGTGAATGGAGACAACCGCGATGCCAGATCATCAAGCGTGTCTGTCAGGCAACGAGCGGCCAGCTCCTATCCAGAGCATAG  
GATCCTCACTCCAGTCTTCCACTCCGATGGCTCCAGAATTTGACGGTTTCAAGCCATTATGAGGAGATCACAGC  
ATGCTCCTCATCCCTTGTTCATGACGGCACGTCCTTGACAAAGGCTGGATCTTACAAGTGTGCTGCTGGCAGGC  
TATACTGGGAGCGCTGTGAAAATCTCTTGAAAGAAAGAAACTGCTCAGACCCCTGGGGCCAGTCATGGTACAGAAAA  
TAACAGGGGCCCTGGGTTATCACGGACGCCATGCTAAATTGGCACCGTGGTCTTTCTTTGTAACAAACTCTATGT  
TCTTAGTGGCAATGAGAAAAGAACTTGGCAGCAGAATGGAGAGTGGTCAGGGAAACAGCCCATCTGCATAAAAGCCTGCCGA  
GAACCAAAGATTTCAGACCTGGTGAAGAGAGTCTCCGATGCCAGGTTGACTCAAGGGAGACACCATTACACCAGCTAT  
ACTCAGGCCCTCAGCAAGCAGAAACTGCAGAGTGCAGGCTTACCAAGAAGCCAGCCCTCCCTGGAGATCTGCCCATGGG  
ATACCAACATCTGCATACCCAGCTCAGATGACTGCATCTCACCCCTCTACCGCCGCCGGCAGCAGCAGGAGGACATGT  
CTGAGGACTGGGAAGTGGACTGGCGGGCACCACCTGCTCATCCCTATGCGGGAAATTGAGAACATCACTGCTCCAAAGA  
CCCAAGGGTTGCGCTGGCGTGGCAGGCCATCTACAGGAGGACCAGCGGGGTGCATGCCAGCCTACAAAGGGAGC  
GTGGTCTCTAGTGTGAGCGGTGCCCTGGTGAATGAGCGACTGTGGTGGTGGCTGCCACTGTGTTACTGACCTGGGAAG  
GTCACCATGATCAAGACAGCAGACCTGAAAGTTGTTGGGAAATTCTACCGGGATGATGACCGGGATGAGAACACATCC  
AGAGCCTACAGATTCTGCTATCATCTGCATCCAACTATGACCCATCCTGCTGATGCTGACATGCCATCCTGAAGCT  
CCTAGACAAGGCCGTATCAGCACCCAGTCCAGCCATCTGCCTGCTGCCAGTCGGATCTCAGCATTCCCTCAGGAG  
TCCACACATCTGTCGCTGGCTGGATGCTCTGGCAGAGCTGAGGAGGCCCTGGCTCAAGAACACACTGCGCTCTGGG  
TGGTCAGTGTGGTGGACTGGCTGCTGTGAGGAGCAGCATGAGGACCATGGCATCCAGTGACTGTCACTGATAACATGTT  
CTGTGCCAGTGGGAAACCCACTGCCCTCTGATATCTGCACTGCAGAGACAGGAGCATGCCGTGTGCTTCCCGGG  
CGAGCATTCTGAGGCCAGCTGGCATCTGATGGACTGGTCAGCTGGAGCTATGATAAAACATGCAAGCCACAGGCTCCA  
CTGCCCTCACCAAGGTGCTGCCCTTAAAGACTGGATTGAAAGAAATGAAACCATGCTCATGCACACTCTTGAGAAG  
TGTTCTGATATCGCTGTACGTGTGTCATTGCGTAAGCAGTGTGGGCTGAAGTGTGATTGGCTGTGAACTTGGCT  
GTGCCAGGGCTCTGACTTCAGGGACAAAACCTCAGTGAAGGGTGAAGTAGACCTCATTGCTGGTAGGCTGATGCCCGTCCA  
CTACTAGGACAGCCATTGGAGATGCCAGGGCTTGCAAGAAGTAAGTTCTTCAAAGAAAGACCATATACAAACCTCTCCA  
CTCCACTGACCTGGGGCTTCCCAACTTCAGTTACGAATGCCATCAGCTTGACCCAGGGAAAGATCTGGGCTTCACTGAG  
GCCCTTGGAGGCTCAAGTTCTAGAGAGGCTGCCGTGGGACGCCAGGGCAGCAGAGCAGCTGGGATGTGGTGCATGCC  
TGTGTACATGCCACAGTACAGTCTGGCTTCCCTCCCTCTGATCACACATTAAATAAGGGTTGGCTTCT  
GAACTACAA  
AA

## **FIGURE 38**

MELGCWTQLGLTFLOLLLSSLPREYTVINEACPGAEWNIMCRECCEYDQIECVCPGKREVVGYT  
IPCCRNEENECDSCLIHPGCTIFENCKSCRNGSWGGTLDDFYVKGFYCAECRAGWYGGDCMRCGQ  
VLRAPKGQILLESYPLNAHCEWTIHAKPGFVIQLRFVMLSLEFDYMCQYDYVEVRDGDNRDGQII  
KRVCGNERPAPIQSIGSSLHVLFHSDGSKNFDGFHAIYEEITACSSSPCFHDGTCVLDKAGSYKC  
ACLAGYTGQRCENLLEERNCSDPGGPVNGYQKITGGPGLINGRHAKIGTVVSFFCNSYVLSNE  
KRTCQQNGEWSGKQPIKACREP KISDLVRRRVLPMQVSRETPLHQLYSAAFSKQKLQSAPTK  
KPALPFGDLPMGYQHLHTQLOQYECISPFYRRLGSSRTCLRTGKWSGRAPSCI PICGKIENTAP  
KTQGLRWPWQAAIYRRRTSGVHDGSLHKGAWFLVCSGALVNERTVVVAHCVTDLGKVTMIKTADL  
KVVLGKFYRDDDREKTIQSLQISAIILHPNYDPILLDADIAILKLLDKARISTRVQPICLAASR  
DLSTS FQESHITVAGWNVLADVRSPGFKN DTLRGVVSVVDSLLCEEQHEDHGI PVS VTDNMFCA  
SWEPTAPS DICTAETGGIAAVSFPGRASPEPRWHLMGLVWSYDKTC SHRLSTAFTKVLPEKDWI  
ERNMK

**Important features of the protein:**

**Signal peptide:**

amino acids 1-23

**EGF-like domain cysteine pattern signature.**

amino acids 260-272

**N-glycosylation sites.**

amino acids 96-100, 279-283, 316-320, 451-455, 614-618

**N-myristoylation sites.**

amino acids 35-41, 97-103, 256-262, 284-290, 298-304, 308-314,  
474-480, 491-497, 638-644, 666-672

**Amidation site.**

amino acids 56-60

**Serine proteases, trypsin family.**

amino acids 489-506

**CUB domain proteins profile.**

amino acids 150-167

## **FIGURE 39**

GGTTCCCTACATCCTCTCATCTGAGAATCAGAGAGCATAATCTTCTACGGGCCGTGATTATTAACGTGGCTTAATC  
TGAAGGTTCTCAGTCATAATTCTTGTGATCTACTGATTGTGGGGCATGGCAAGGTTGCTTAAAGGAGCTGGCTGG  
TTTGGGCCCTGTAGCTGACAGAAGGTGGCAGGGAGAATGCAGCACACTGCTGGAGAATGAAGGCCTCTGTTGC  
TGGTCTTGCCCTGGCTAGTCAGTCATACTACATTGACAATGTGGCAACCTGCACCTCTGTATTCAAGACTCTGTA  
AAGGTGCTCCCACGCGCCTGACCAAAGATAGGAAGAGGCCTACAAGATGGCTGTCCAGACGGCTGTGCGAGCC  
TCACAGCCACGGCTCCCTCCCCAGAGGTTCTGCAGCTGCCACCATCTCTTAATGACAGACGAGCCTGGCTAGACA  
ACCCCTGCCTACGTGTCTCGGCAGAGGACGGGCAGCCAGCAATCAGCCCAGTGGACTCTGGCCGGAGCAACCGAAGTA  
GGGCACGGCCCTTGAGAGATCCACTATTAGAACGATCATTTAAAAAAATAATCGAGCTTGAGTGTCTCGAA  
GGCAAAGAGCGGGAGTGCAGTTGCCAACCATGCCGACCGGGCAGGGAAAATTCTGAAAACACCACTGCCCTGAAG  
TCTTCCAAGGTTGTACCCACCTGATTCCAGATGGTGAATTACACAGCATCAAGATCAATCGAGTAGATCCCAGTGAAA  
GCCCTCTCTATTAGGCTGGGGAGGTAGCAGAACCCCCACTGGTCCATATCATTATCCAACACATTATCGTGTGGGG  
TGATCGCCAGAGACGCCGGCTACTGCCAGGAGACATCATTCTAAAGGTCACAGGGATGGACATCAGCAATGTCCCTC  
ACAACATACGCTGTGCGTCTCTGCCAGCCCTGCCAGGTGCTGTGGCTGACTGTGATGCGTGAACAGAAGTCCGCA  
GCAGGAACAAATGGACAGGCCCGGATGCCCTACAGACCCCGAGATGACAGCTTCATGTGATTCACAAAGTAGCC  
CCGAGGAGCAGCTTGAATAAAACTGGTGGCAAGGTGGATGAGCTGGGTTTCTATCTCAATGCTGGATGGCG  
GTGTGGCATATCGACATGGTCAGCTGAGGAGAATGACCGTGTGTTAGCCATCAATGGACATGATCTCGATATGGCA  
GCCAGAAAGTGGCGCTCATCTGATTCCAGGCCAGTGAAGAGACGTGTTACCTCGTGTCCGCCAGGTTGGCAGC  
GGAGCCCTGACATCTTCAGGAAGCCGGTGGAAACAGCAATGGCAGCTGGTCCCCAGGGCAGGGAGAGGAGCAACA  
CTCCCAAGCCCTCCATCTACAAATTACTGTGATGAGAAGGTGGAAATATCACAAAGACCCCGTGAATCTCTG  
GCATGACCGTGCAGGGGAGCATCACATAGAGAATGGGATTGCTATCTATGTCATCAGTGTGAGCCGGAGGAG  
TCATAAGCAGAGATGGAAGAATAAAACAGGTGACATTGTGATGTGGATGGGTGCAACTGACAGAGGTGAGC  
GGAGTGAGGAGCTGGCATATTGAAAGAACATCCTCGATAGTACTCAAAGCTTGGAAAGTCAAAGAGTATGAGC  
CCCAGGAAGACTGCAGCAGCCAGCAGCCCTGGACTCCAACACACATGGCCCCACCCAGTGACTGGTCCCCATCCT  
GGGTCACTGGCTGGAAATTACACGGTGTGATAACTGTAAAGATATTGTATTACAGAAGAACACAGCTGGAGTC  
TGGCTTCTGCATTGAGGAGTTATGAAAGAACATGAAACATGGAAACCTTTTCTATCAAATCATTGTTGAAGGAA  
CACCAAGCATACAATGATGGAAGAATTAGATGTGGTGTATTCTTCTGCTGTCATGGTAGAAGTACATCAGGAATGA  
TACATGCTGCTGGCAAGACTGCTGAAAGAACTTAAAGGAAGAATTACTCTAAACTATTGTTCTGGCCTGGCACTT  
TTTTATAGAATCAATGATGGTCAAGGGAAACAGAAAAACAGAAAATCACAAATAGGCTAAGAAGTGAACACTATATTATC  
TTGTCAGTTTATATTAAAGAAAGAACATTGTAAGGAAAGTCAAGGAAAGTATGATCATCTAAATGAAAGCCAGTT  
ACACCTCAGAAAATGATTCCAAAAAAATTAAACACTAGTTTTCTAGTGTGGAGGATTCTCATTACTCTAC  
AACATTGTTATTTTCTATTCAATAAAAGCCCTAAACAAACTAAAATGATTGATTGTATAACCCACTGAATT  
CAAGCTGATTAAATTTAAATGGTATATGCTGAAGTCTGCCAAGGGTACATTATGCCATTAAATTACAGCT  
AAAATTTTAAATGCATTGCTGAGAACAGTTGCTTCATCAAACAAAGAATAATTTTCAAGAAGTTAAA

## **FIGURE 40**

MKALLLLVLPWLSPANYIDNVGNLHFLYSELCKGASHYGLTKDRKRRSQDGCPDCASLTATAPS  
PEVSAATISLMTDEPGLDNPAYVSSAEDGQPAISPVDGRSNRTRARPFERSTIRSRFSKKINR  
ALSVLRRTKSGAVANHADQGRENSENTTAPEVFPRLYHLIPDGEITSIKINRVDPSESLSIRLV  
GGSETPLVHIIIQHIYRDGVIARDGRLLPGDIILKVNNGMDISNVPHNYAVRLLRQPCQVLWLTVM  
REQKFRSRNNGQAPDAYPRDDSFHVILNKSSPEEQLGIKLVRKVDEPGVFIIFNVLDGGVAYRHG  
QLEENDRVLAINGHDLRYGSPESAHLIQASERRVHLVVSQRQSPDIFQEAGWNSNGSWSPG  
PGERSNTPKPLHPTITCHEKVVNIQKDPGESLGMTVAGGASHREWDLPIYVISVEPGGVISRDGR  
IKTGDILLNVDGVELTEVSRSEAVALLKRTSSSIVLKALEVKEYEPQEDCSSPAALDSHNHMAPP  
SDWSPSWVMWLELPRLYNCKDIVLRRNTAGSLGFCIVGGYEEYNGNKPFFIKSIVEGTPAYNDG  
RIRCGDILLAVNGRSTSGMIHACLRLLKELKGRITLTIVSWPGTFL

**Important features:**

**Signal peptide:**

amino acids 1-15

**N-glycosylation sites.**

amino acids 108-112, 157-161, 289-293, 384-388

**Tyrosine kinase phosphorylation sites.**

amino acids 433-441, 492-500

**N-myristoylation sites.**

amino acids 51-57, 141-147, 233-239, 344-350, 423-429, 447-453,  
467-473, 603-609

## FIGURE 41

ACCAAGGCATTGTATCTTCAGTTGTCATCAAGTCGCAATCAGATTGGAAAAGCTCAACTGAGCTTT  
CTTGCCTGCACTGAAGCAGAGAGATAGATATTATTACACGTAATAAAAACATGGGCTCAACCTGACT  
TTCCACCTTCCTACAAATTCCGATTACTGTTGCTGACTTGTGCCTGACAGTGGTTGGTGGC  
CACCAAGTAACACTTCGTGGGTGCCATTCAAGAGATTCTAAAGCAAAGGAGTCATGGCTAATTCC  
ATAAGACCCCTCATTTGGGGAAAGGGAAAAACTCTGACTAATGAAGCATTCCACGAAGAAGGTAGAACTT  
GACAACGTCTTCTGTGCTCCTTACCTCAGAGGCCAGAGCAAGCTCATTCAAACCAAGATCTCAC  
TTTGGAAAGAGGTACAGGCAGAAAATCCCAAAGTGTCCAGAGGCCGTATGCCCTCAGGAATGAAAG  
CTTTACAGAGGGTCGCCATCCTCGTCCCCACCGGAACAGAGAGAAACACCTGATGTACCTGCTGGAA  
CATCTGCATCCCTCCTGCAGAGGCAGCAGCTGGATTATGGCATCTACGTCACTCCACCAGGCTGAAGG  
TAAAAAGTTAATCGAGCAAACCTCTGAAATGTGGCTATCTAGAAGCCCTCAAGGAAGAAAATTGGG  
ACTGCTTATATTCCACGATGTGGACCTGGTACCCGAGAATGACTTAACTTACAAGTGTGAGGAG  
CATCCCAAGCATCTGGTGGTGGCAGGAACAGCACTGGTACAGGTTACGTTACAGTGGATATTGG  
GGGTGTTACTGCCCTAAGCAGAGAGCAGTTTCAAGGTAATGGATTCTCTAAACAACACTGGGAT  
GGGGAGGCGAAGACGATGACCTCAGACTCAGGGTTGAGCTCCAAAGAATGAAAATTCCCGCCCCCTG  
CCTGAAGTGGTAAATATACAATGGTCTTCCACACTAGAGACAAAGGCAATGAGGTGAACGCAGAACG  
GATGAAGCTTACACCAAGTGTACGAGTCTGGAGAACAGATGGTTGAGTAGTTGTTCTTATAAT  
TAGTATCTGTGGAACACAATCCTTATATATCAACATCACAGTGGATTCTGGTTGGTGCATGACCC  
TGGATCTTGGTGTGTTGGAAAGAACTGATTCTTGTGCAATAATTGGCTAGAGACTTCAA  
ATAGTAGCACACATTAAGAACCTGTTACAGCTCATTGTTGAGCTGAATTTCCTTTGTATTCT  
TAGCAGAGCTCTGGTGTAGTGTAGAGTATAAACAGTTGTAACAAGACAGCAGCTTCTTAGTCATTGAT  
CATGAGGGTTAAATATTGTAATATGGAACTTGAAGGACTTATATAAAAGGATGACTCAAAGGATAA  
AATGAACGCTATTGAGGACTCTGGTGAAGGAGATTAAATTGAGTAATATATTATGGGAT  
AAAAGGCCACAGGAAATAAGACTGCTGAATGTCTGAGAGAACAGAGTTGTTCTCGTCCAAGGTAGAA  
AGGTACGAAGATAACAACTGTTATTCACTTATCCTGTACAATCATCTGTAAGTGGTGGTGTAGGT  
GAGAAGGGTCCACAAAAGAGGGAGAAAAGGCGACGAATCAGGACACAGTGAACCTGGGAATGAAGA  
GGTAGCAGGAGGGTGGAGTGTGGCTGCAAAGGCAGCAGTAGCTGAGCTGGTTGCAGGTGCTGATAGC  
CTTCAGGGAGGACCTGCCAGGTATGCCCTCCAGTGTGATGCCACCAGAGAAATACATTCTTATTAGT  
TTTAAAGAGTTTGTAAATGATTTGTACAAGTAGGATATGAATTAGCAGTTACAAGTTACAT  
ATTAACATAATAATATGTCTATCAAATACCTCTGTAGAAAATGTGAAAAAGCAAAA

## **FIGURE 42**

MGFNLTFHLSYKFRLLLLTLCLTVVGWATSNYFVGAIQEIPKAKEFMANFHKTLLGKGKTLTN  
EASTKKVELDNCPSVSPYLRGQSKLIFKPDLTLEEVQAENPKVSRGRYRPQECKALQRVAILVPH  
RNREKHLMLLEHLHPFLQRQQLDYGIYVIHQAEKKFNRAKLLNVGYLEALKEENWDCFI FHDV  
DLVPENDFNLYKCEEHPKHLVGRNSTGYRLRYSGYFGGVTA LSREQFFKVNGFSNNYWGWGGED  
DDLRLRVELQRMKISRPLPEVGKYTMVFHTRDKGNEVNAERMKLLHQVSRVWRTDGLSSCSYKLV  
SVEHNPLYINITVDFWFGA

**Important features:**

**Signal peptide:**

amino acids 1-27

**N-glycosylation sites.**

amino acids 4-8, 220-224, 335-339

**Xylose isomerase proteins.**

amino acids 191-202

## **FIGURE 43**

GCTCAAGACCCAGCAGTGGGACAGCCAGACAGACGGCACGGATGGCACTGAGCTCCAGATCTGGG  
CCGCTTGCCTCCTGCTCCTCCTCGCCAGCCTGACCAGTGGCTCTGTTCCCACAAACAG  
ACGGGACAACCTGAGCTGCAACCCAGGACAGAGCTGGAGCCAGGGCAGCTGGATGCCAT  
GTTCCAGAGGCGAAGGGAGGCGAGACACCCACTTCCCACATCTGCATTTCTGCTGCGGCTGCTGTC  
ATCGATCAAAGTGTGGATGTGCTGCAAGACGTAGAACCTACCTGCCCTGCCCCGTCCCCCTCCC  
TTCCTTATTATTCTGCTGCCAGAACATAGGTCTTGAATAAAATGGCTGGTTCTTTGTTT  
TCCAAA  
AAAAAAAAAAAAAAAAAAAAAAA

## FIGURE 44

MALSSQIWAACLLLLLTLASLTSGSVFPQQTGQLAELQPQDRAGARASWMPMFQRRRRDTHFPI  
CIFCCGCCHRSKCGMCKT

**Important features:**

**Signal peptide:**

amino acids 1-24

**cAMP- and cGMP-dependent protein kinase phosphorylation site.**

amino acids 58-59

**N-myristoylation site.**

amino acids 44-50

**Prokaryotic membrane lipoprotein lipid attachment site.**

amino acids 1-12

## **FIGURE 45**

GTGGCTTCATTCAGTGGCTGACTTCCAGAGAGCAATATGGCTGGTCCCCAACATGCCTCACCC  
TCATCTATATCCTTGGCAGCTCACAGGGTCAAGCAGCCTCTGGACCCGTGAAAGAGCTGGTCGGT  
TCCGTTGGTGGGGCCGTGACTTCCCCCTGAAGTCAAAGTAAAGCAAGTTGACTCTATTGTCTG  
GACCTTCAACACAACCCCTCTTGTACCACAGCCAGAAGGGGGCACTATCATAGTGACCCAAA  
ATCGTAATAGGGAGAGAGTAGACTTCCCAGATGGAGGCTACTCCCTGAAGCTCAGCAAATGAAG  
AAGAATGACTCAGGGATCTACTATGTGGGATATACAGCTCATCAGCAGCCCTCCACCCA  
GGAGTACGTGCTGCATGTCTACGAGCACCTGCTAAAGCCTAAAGTCACCATGGGTCTGCAGAGCA  
ATAAGAATGGCACCTGTGACCAATCTGACATGCTGCATGGAACATGGGAAGAGGATGTGATT  
TATACTGGAAGGCCCTGGGCAAGCAGCCAATGAGTCCCATAATGGGTCCATCCTCCCCATCTC  
CTGGAGATGGGAGAAAGTGATATGACCTTCATCTGCCAGGAAGGTGCTGCTGATGACCCAGATTCCCTCATG  
TCTCAAGCCCCATCCTGCCAGGAAGCTGTGAAGGTGCTGCTGATGACCCAGATTCCCTCATG  
GTCCTCCTGTGTCTCCTGTTGGTGCCTCCTGCTCAGTCTTTGACTGGGTATTCTTG  
GTTTCTGAAGAGAGAGACAAGAAGAGTACATTGAAGAGAAGAAGAGTGGACATTGTCGGG  
AAACTCCTAACATATGCCCTATTCTGGAGAGAACACAGAGTACGACACAATCCCTCACACTAAT  
AGAACAAATCCTAAAGGAAGATCCAGCAAATACGGTTACTCCACTGTGGAAATACGAAAAAGAT  
GGAAAATCCCCACTCACTGCTCACGATGCCAGACACACCAAGGCTATTGCCTATGAGAATGTTA  
TCTAGACAGCAGTGCACTCCCCTAAGTCTGCTCA

## **FIGURE 46**

MAGSPTCLTLIYILWQLTGSAASGPVKELVGSGAVTFPLSKVKQVDSIVWTFTNTPLVTIQP  
EGGTIIVTQNRNRERVDFPDGGYSLKLSKKNDSGIYYVGIYSSSLQQPSTQEVVLHVYEHLSK  
PKVTMGLQSNKNGTCVTNLTCMEHGEEDIYTWKALGQAANESHNGSILPISWRWGESDMTFIC  
VARNPVSRNFSSPILARKLCEGAADDPDSSMVLLCLLVLVPLLLSLFVLGLFLWFLKRERQEEYIE  
EKKRVDICRETPNICPHSGENTEYDTIPHTNRTILKEDPANTVYSTVEIPKKMENPHSLLTMPDT  
PRLFAYENVI

**Important features:**

**Signal peptide:**

amino acids 1-22

**Transmembrane domain:**

amino acids 224-250

**Leucine zipper pattern.**

amino acids 229-251

**N-glycosylation sites.**

amino acids 98-102, 142-146, 148-152, 172-176, 176-180, 204-208,  
291-295

## **FIGURE 47**

GGCTCGAGCGTTCTGAGCCAGGGTGACCATGACCTGCTGCGAAGGATGGACATCCTGCAATGG  
ATTCAGCCTGCTGGTCTACTGCTGTTAGGAGTAGTTCTCAATGCGATAACCTCTAATTGTCAGCT  
TAGTTGAGGAAGACCAATTTCTCAAAACCCATCTCTGCTTGAGTGGTGGTCCCAGGAATT  
ATAGGAGCAGGTCTGATGCCATTCCAGCAACAACAATGTCCTTGACAGCAAGAAAAAGAGCGTG  
CTGCAACAACAGAACGAACTGGAATGTTCTTCATCATTTCAGTGTGATCACAGTCATTGGTGCTC  
TGTATTGCATGCTGATATCCATCCAGGCTCTCTAAAGGTCTCATGTGTAATTCTCCAAGC  
AACAGTAATGCCAATTGTAATTTCATTGAAAAACATCAGTGACATTCCAGAACATCCTCAA  
CTTGCAGTGGTTTCAATGACTCTTGTGCACCTCCTACTGGTTCAATAAACCCACCAGTAACG  
ACACCATGGCGAGTGGCTGGAGAGCATCTAGTTCCACTTCGATTCTGAAGAAAACAAACATAGG  
CTTATCCACTCTCAGTATTTAGGTCTATTGCTTGAAATTCTGGAGGTCTGTTGGGCT  
CAGTCAGATAGTCATCGGTTCCCTGGCTGTCGTGAGTCTTAAGCGAAGAAGTCAAATTG  
TGTAGTTAATGGGATAAAATGTAAGTATCAGTAGTTGAAAAA

## **FIGURE 48**

MTCCEGWTSCNGFSLLVLLLGVLNAIPLIVSLVEEDQFSQNPISCFEWWFPGIIGAGLMAIPA  
TTMSLTARKRACCNNRTGMFLSSFFSVITVIGALYCMLISIQALLKGPLMCNSPSNSNANCEFSL  
KNISDIHPESFNLQWFFNDSCAPPTGFNKPTSNDTMASGWRASSFHFDSEENKHRLIHFSVFLGL  
LLVGILEVLFGLSQIVIGFLGCLCGVSKRRSQIV

**Important features:**

**Transmembrane domains:**

amino acids 10-31 (type II), 50-72, 87-110, 191-213

**N-glycosylation sites.**

amino acids 80-84, 132-136, 148-152, 163-167

**cAMP- and cGMP-dependent protein kinase phosphorylation site.**

amino acids 223-227

**N-myristylation sites.**

amino acids 22-28, 54-60, 83-89, 97-103, 216-222

**Prokaryotic membrane lipoprotein lipid attachment site.**

amino acids 207-218

**TNFR/NGFR family cysteine-rich region protein.**

amino acids 4-12

## **FIGURE 49**

ATCCGTTCTCTGCGCTGCCAGCTCAGGTGAGCCCTGCCAAGGTGACCTCGCAGGACACTGGTGA  
AGGAGCAGTGAGGAACCTGCAGAGTCACACAGTTGCTGACCAATTGAGCTGTGAGCCTGGAGCAG  
ATCCGTGGCTGCAGACCCCCGCCCCAGTGCCTCTCCCCCTGCAGCCCTGCCCTCGAACTGTGA  
**CATGGAGAGAGTGA**CCCTGGCCCTCTACTATGACTGGAAAAACCTGCAGCTGAGCGGACTGATC  
CATTTGCCAATAAAGACGATCCCTCTACTATGACTGGAAAAACCTGCAGCTGAGCGGACTGATC  
TGC GGAGGGCTCTGGCCATTGCTGGGATCGCGCAGTTCTGAGTGGCAAATGCAAATACAAGAG  
CAGCCAGAAGCAGCACAGTCCGTACCTGAGAAGGCCATCCACTCATCACTCCAGGCTCTGCCA  
CTACTTGCTGACACAGGACTGGCCTCCAGGGATGGCTGAAGCCTAACACTGGCCCCAGCACC  
TCCTCCCCCTGGGAGGCCTTATCCTCAAGGAAGGACTTCTCTCCAAGGGCAGGCTGTTAGGCCCC  
TTCTGATCAGGAGGCTTCTTATGAATTAAACTCGCCCCACCACCCCCCTCA

## **FIGURE 50**

MERVTLALLLLAGLTALLEANDPANKDDPFYYDWKNLQLSGLICGGLLAIAGIAAVLSGKCKYKS  
SQKQHSPVPEKAIPLITPGSATTC

**Important features:**

**Signal peptide:**

amino acids 1-16

**Transmembrane domain:**

amino acids 36-59

**N-myristoylation sites.**

amino acids 41-47, 45-51, 84-90

**Extracellular proteins SCP/Tpx-1/Ag5/PR-1/Sc7.**

amino acids 54-67

## **FIGURE 51**

GTGGACTCTGAGAAGCCCAGGCAGTTGAGGACAGGAGAGAGAAGGCTGCAGACCCAGAGGGAGGG  
AGGACAGGGAGTCGAAGGAGGGACAGAGGAGGGCACAGAGACGCAGAGCAAGGGCGGCAAGG  
AGGAGACCTGGTGGAGGAAGACACTCTGGAGAGAGAGGGCTGGCAGAGATGAAGTCCAG  
GGGCCCCCTGGCCTGCCTCCTGCTGGCCCTCTGCCTGGCAGTGGGAGGCTGGCCCTGCAGAG  
CGGAGAGGAAAGCAGTGGACAAATATTGGGGAGGCCCTGGACATGGCCTGGAGACGCCCTGA  
GCGAAGGGTGGAAAGGCCATTGGCAAAGAGGCCGGAGGGCAGCTGGCTCTAAAGTCAGTGAG  
GCCCTGGCCAAGGGACCAGAGAAGCAGTGGCACTGGAGTCAGGCAGGTTCCAGGCTTGGCAG  
AGCAGATGCTTGGCAACAGGTGGGAAGCAGCCATGCTCTGGAAACACTGGCAGCAGA  
TTGGCAGACAGGCAGAAGATGTCATTGACACGGAGCAGATGCTGTCCGCGGCTCTGGCAGGG  
GTGCCTGGCACAGTGGCTGGAAACTCTGGAGGCCATGGCATCTTGGCTCTAAGGTGG  
CCTTGGAGGCCAGGGCAAGGGCAATCCTGGAGGTCTGGGACTCCGTGGTCCACGGATAACCCG  
GAAACTCAGCAGGCAGCTTGAATGAATCCTCAGGGAGCTCCCTGGGTCAAGGAGGCAATGGA  
GGGCCACCAAACCTTGGACCAACACTCAGGGAGCTGTGGCCAGGCTGGCTATGGTCAGTGAG  
AGCCAGCAACCAGAAATGAAGGGTGCACGAATCCCCACCATCTGGCTCAGGTGGAGGCTCCAGCA  
ACTCTGGGGAGGCAGCGGCTCACAGTGGCAGCAGTGGCACTGGCAGCAATGGTACAAACAC  
AATGGCAGCAGCAGTGGTGGCAGCAGCAGTGGCAGCAGCAGTGGCAGCAGTGGCAGCAG  
TGGCGCAGCAGTGGTGGCAGCAGTGGCAACAGTGGTGGCAGCAGAGGTGACAGCGGAGTGG  
CCTCCTGGGATCCAGCACCGGCTCCTCCTGGCAACCACGGTGGAGCGGGAGGAAATGGA  
CATAAACCCGGGTGTGAAAGCCAGGGAAATGAAGCCCCGGAGCGGGGAATCTGGGATTCAAGG  
CTTCAGAGGACAGGGAGTTCCAGCAACATGAGGGAAATAAGCAAAGAGGGCAATGCCCTCTG  
GAGGCTCTGGAGACAATTATCGGGGCAAGGGTCAGCTGGGAGTGGAGGAGGTGACGCTGTT  
GGTGGAGTCATACTGTGAACCTCTGAGACGGTCTCTGGGATGTTAACCTTGACACTTCTGGAA  
GAATTTAAATCCAAGCTGGTTCATCAACTGGGATGCCATAAACAAAGGACAGAGAAGCTCTC  
GCATCCCGTGACCTCCAGACAAGGAGCCACAGATTGGATGGAGCCCCCACACTCCCTCTTAA  
AACACCACCCCTCTCATCACTAATCTCAGCCCTGGCCTTGAAATAACCTTAGCTGCCCAACAAA  
AA  
AAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAA

## **FIGURE 52**

MKFQGPLACLLLALCLGSGEAGPLQSGEESTGTNIGEALGHGLGDALSEGVGKAIGKEAGGAAGSKVS  
EALGQGTREAVGTGVRQVPGFGAADALGNRVGEAAHALGNTGHEIGRQAEDVIRHGADAVRGSWQGVP  
GHSGAWETSGGHGIFGSQGGLGGQGQGNPGGLGTPWVHYPGNSAGSFGMNPQGAPWGQGGNGGPPNF  
GTNTQGAVAQPGYGSVRASNQNEGCTNPPSGSGGGSSNSGGSGSQSGSSGSGSMNDNNNGSSSGS  
SSGSSSSGSSGGSSGGSSGSSG  
ARGSGESGIQGFRGQGVSSNMREISKEGNRLGGSGDNYRGQGSSWGSGGDAVGGVNTVNSETSPGM  
FNFDTWFKNFKSKLGFINWDAINKDQRSSRIP

**Signal peptide:**

amino acids 1-21

**N-glycosylation site.**

amino acids 265-269

**Glycosaminoglycan attachment site.**

amino acids 235-239, 237-241, 244-248, 255-259, 324-328, 388-392

**Casein kinase II phosphorylation site.**

amino acids 26-30, 109-113, 259-263, 300-304, 304-308

**N-myristoylation site.**

amino acids 17-23, 32-38, 42-48, 50-56, 60-66, 61-67, 64-70, 74-80,  
90-96, 96-102, 130-136, 140-146, 149-155, 152-158, 155-161,  
159-165, 163-169, 178-184, 190-196, 194-200, 199-205, 218-224,  
236-242, 238-244, 239-245, 240-246, 245-251, 246-252, 249-252,  
253-259, 256-262, 266-272, 270-276, 271-277, 275-281, 279-285,  
283-289, 284-290, 287-293, 288-294, 291-297, 292-298, 295-301,  
298-304, 305-311, 311-317, 315-321, 319-325, 322-328, 323-329,  
325-331, 343-349, 354-360, 356-362, 374-380, 381-387, 383-389,  
387-393, 389-395, 395-401

**Cell attachment sequence.**

amino acids 301-304

## **FIGURE 53**

GGAGAAGAGGTTGTGGGACAAGCTGCTCCGACAGAAGGGATGTCGCTGCTGAGCCTGCCCTGG  
CTGGGCTCAGACCGGTGGCAATGTCCTGGCTACTCCCTGCTGCTGGTTGGGCTCCAGTGGCT  
ACTCGCCCGCATCCTGGCTTGACCTATGCCCTATAACAACTGCCGCCGGCTCCAGTGTTC  
CACAGCCCCAAAACGGAACGGTTGGGTACCTGGGCTGATCACTCCTACAGAGGAGGGC  
TTGAAGGACTCGACCCAGATGTCGCCACCTATTCCCAGGGCTTACGGTATGGCTGGTCCC  
CATCCCCCTCATCGTTTATGCCACCCGACACCATCCGGTCTATACCAATGCCCTAGCTGCC  
TTGCACCCAAGGATAATCTCTCATCAGGTTCTGAAGCCCTGGCTGGAGAAGGGATACTGCTG  
AGTGGCGGTGACAAGTGGAGGCCACCGTCGGATGCTGACGCCCTTCCATTCAACATCCT  
GAAGTCCTATATAACGATCTTCAACAAGAGTGCACAAACATCATGCTTGACAAGTGGCAGCACCTGG  
CCTCAGAGGGCAGCAGTCGCTGGACATGTTGAGCACATCAGCCTCATGACCTGGACAGTCTA  
CAGAAATGCATCTTCAGCTTGACAGCCATTGTCAGGAGAGGCCAGTGAATAATTGCCACCAT  
CTTGGAGCTCAGTGCCTTGAGAGAAAAGAAGCCAGCATATCCTCCAGCACATGGACTTCTGT  
ATTACCTCTCCATGACGGGCGCGCTTCCACAGGGCCTGCCGCTGGTGCATGACTCACAGAC  
GCTGTCATCCGGGAGCGCGTGCACCCCTCCCCACTCAGGTATTGATGATTTTCAAAGACAA  
AGCCAAGTCCAAGACTTGGATTCATTGATGTGCTTGCTGAGCAAGGATGAAGATGGAGG  
CATTGTCAGATGAGGATAAAAGAGCAGAGGCTGACACCTCATGTTGGAGGCCATGACACCACG  
GCCAGTGGCCTCTCCTGGTCTGTACAACCTGCGAGGCACCCAGAAATACCAGGAGCGTGC  
ACAGGAGGTGCAAGAGCTCTGAAGGACCCGATCTAAAGAGATTGAATGGGACGACCTGCC  
AGCTGCCCTCCTGACCATGTGCGTGAAGGAGAGCCTGAGGTTACATCCCCAGCTCCCTCATC  
TCCCAGTGCACCCAGGACATTGTTCTCCAGATGCCGAGTCATCCCCAAAGGCATTACCTG  
CCTCATCGATATTATAGGGTCCATCACAAACCCAACTGTGTCGGGGATCCTGAGGTCTACGACC  
CCTTCCGCTTGACCCAGAGAACAGCAAGGGAGGTACCTCTGGGTTTATTCCCTTCTCCGCA  
GGGCCCAGGAACGTGACATGGGCAAGGCAGACACTGAGCCCCGAGGAAGCTGGAATTGATCATGC  
GCGCCGAGGGCGGGCTTGGCTGCGGGTGGAGCCCTGAATGTAGGCTTGCAGATTTCTGAC  
CCATCCACCTGTTTTGCAGATTGTCATGAATAAACGGTGCTGTCAAA

## **FIGURE 54**

MSLLSLPWGLRPVAMSPWLLLLVVGSWLLARILAWTYAFYNNCRLQCFPQPKRNWFWGHLG  
LITPTEEGLKDSTQMSATYSQGFTVWLGPPIIPFIVLCHPDTIRSITNASAAIAPKDNLFIRFLKP  
WLGEGLLGGDKWSRHRRMLTPAFHFNILKSYITIFNKSANIMLDKWQHLASEGSSRLDMFEHI  
SILMTLDSLQKCIFSFDSHCQERPSEYIATILELSALVEKRSQHILQHMDFLYYLSHDGRRFHRAC  
RLVHDFTDAVIRERRRLPTQGIDDFFKDKAKSKTLDFIDVLLSKDEDGKALSDEDIRAEADTF  
MFGGHDTTASGLSWVLYNLRHPEYQERCQEVQELLKDRDPKEIEWDDLAQLPFLTMCVKESLR  
LHPPAPFISRCCTQDIVLPDGRVIPKGITCLIDIIGVHHNPTVWPDPPEVYDPFRFPENSKGSP  
LAFIPFSAGPRNCIGQAFAMAEMKVVLALMLHFRFLPDHTEPRRKLELIMRAEGGLWLRVEPLN  
VGLQ

**Important features:**

**Transmembrane domains:**

amino acids 13-32 (type II), 77-102

**Cytochrome P450 cysteine heme-iron ligand signature.**

amino acids 461-471

**N-glycosylation sites.**

amino acids 112-116, 168-172

## **FIGURE 55**

ATCGCATCAATTGGGAGTACCATCTCCTCATGGGACCAGTGAAACAGCTGAAGCGAATGTTGA  
GCCTACTCGTTGATTGCAACTATCATGGGCTGTTGTTGCACTTACCCCTGTGTTGCCT  
TTTGGTGGCATAACAAGGGACTTGCACTTATCTTCTGCATTTGCAGTCTTGGCATTGACGTGG  
TACAGCCTTCCTTCATACCATTGCAAGGGATGCTGTGAAGAAGTGTGTTGCCGTGTCTGC  
ATAATTCATGCCAGTTATGAAGCTTGAAGGCACTATGGACAGAAGCTGGTGGACAGTTT  
GTAACATCTCGAACACCTCTGCTTACAGACATGTGCCCTTATCTTGCAGCAATGTGTTGCTT  
GTGATTGAAACATTGAGGGTTACTTTGGAAGCAACAATACATTCTCGAACCTGAATGTCAGTA  
GCACAGGATGAGAAGTGGGTTCTGTATCTGTGGAGTGGAAATCTCCTCATGTACCTGTTCTC  
TCTGGATGTTGTCCCCTGAATTCCCATGAATACAAACCTATTCAACAGCAACAGCAAAAAAAAAAAA  
AAA

## **FIGURE 56**

MGPVKQLKRMFEPTRLIATIMVLLCFALTLCASFWWHNGLALIFCILQSLALTWYSLSFIPFAR  
DAVKKCFAVCLA

**Important features:**

**Signal peptide:**

amino acids 1-33

**Type II fibronectin collagen-binding domain protein.**

amino acids 30-72

## FIGURE 57

CGGCTCGAGCTCGAGCGAATCGGCTCGAGGGGCAGTGGAGCACCCAGCAGGCCAACATGCTCTGCTGTGCCTG  
TACGTGCCGTCATCGGGAAAGCCCAGACCGAGTTCCAGTACTTGAGTCGAAGGGCTCCCTGCCAGCTGAAGTCC  
ATTTCAAGCTCAGTGTCTCATCCCCCTCCAGGAATTCTCACCTACCGCACTGGAACAGAAAATTGACAAGCT  
GGAGATAAGGACCTTGTAGGGCAGCTAGACTTTGAAGAATTGTCATTATCTCAAGATCATGAGAAGAAGCTGAGG  
CTGGTGTAAAGATTTGGACAAAAGAATGTGGACGCTAGGAGGAGATCATGAGTCCCTGCGGGACTTG  
GGACTCAAGATATCTGAACAGCAGGCCAAAATTCTCAAGAGCATGGAAAAACGGCACGATGACCACGACTGG  
AACAGTGGAGAGACTACCACTCCTCACCCGATGGAAAATCCTGGAGATCATCTACTGGAAAGCATCCACG  
ATCTTGATGTGGTGAAGAATCTAACGGTCCCGATGAGTTACAGTGGAGGAGGGAGACGGGATGTGGTGGAGA  
CACCTGGTGCAGGAGGTGGGGCAGGGCGTATCCAGAACCTGCACGGCCCCCTGGACAGGCTCAAGGTGCTCATG  
CAGGTCCATGCCATCCCAGAACATGGCATCTGGTGGCTTCACTCAGATGATTGAGAAGGGGGCCAGG  
TCACCTGGCGGGCAATGGCATCACGCTCTAAACATGGCCAACTGCCCACATGCCATCAAATTGAGCAG  
ATCAAGGCCCTGTGCTAGTGGAGGACTCTGAGGATTCAGCAGGGCTGGCAGGGCTCTGGCAGGGCC  
ATCGCCCAGAGCAGCATCACCAATGGAGTCTGAAAGACCCGATGGCGTGGGAAGACAGGCCAGTACTCAGGA  
ATGCTGGACTGCGCCAGGAGATCTGGCAGAGAGGGGTGGCCCTTCTACAAAGGCTATGTCCTAACATGCTG  
GGCATCATCCCTATGCCGATCAGCTTCACTCAGACGCTCAAGAATGCTGGCTGCAGCACTATGAGTG  
AACAGCAGGCCAGGGCTGTCTCTGGCACCAGTGGCTGGCAGCTGGCAGCTGGCAGCTAC  
CCCCCTGGCCCTAGTCAGGACCCGGATGAGGCGAACGCTTATTAGGGCGTCCGGAGGTGACCATGAGCAGCCTC  
TTCAAACATATCTGGGAGGGCTTCGGCTGATCAGGGGCTGGCCCAACTTCTGAAAGGTGATCCCA  
GCTGTGAGCATCAGCTACGTGGTCTACAGAACCTGAAGATCACCTGGCGTGCAGTCGGTGACGGGGGGAGGGC  
CGCCCGGAGTGGACTCGCTGATCTGGGGCAGCCTGGGTGAGCCATCTCATTCTGTGAATGTGCCAACACT  
AAGCTGTCAGGCAAGCTGTGAAAACCTTACAGCAGCCGAGGGGGAGAGCTGGCAGGCCAGGGCTT  
GTCTGCTGACCCAGCAGCACCTCTGGTCTGGCTCAGGAAGACACAGGATTTAGGGTCCAGGGTCAAGCAGG  
CTCCGGGCTCACATGTAAGGACAGGACATTTCAGCTGGCCAACTGAGCTTGGAGCTGGAGCCGGCT  
TAGTTCTCCATTTCACCCCTGAGCCAGCTGGCCACGGCCCTGGCTGCTGCGCTCATCTCCCTGTG  
CCTCTGCTGCGCTGCTGCTGAGCTAAGGAGGGCTACAGCCACATCCCACCCCTGTCCAATCCC  
ATAATCCATGAAAGGTGAGGTACAGCTGGCTGAGGCTGACTTCCAGGCAACTACAGCATTGACGCCACTGG  
TGTGAAGGAAGAGGAAGGGATCTGGCTTGTGCTACTGGCATCTGAGCTGGCTGGGGCTCTGGGAG  
CTTGGGAGTGCAGGGGGCTGGGCTGGCTGGCTGGCTGACAGAGGCAACTGCTGGGGCTCATGGCTCTGGAGCT  
GCCCTGGACCTGTCAGGATGGGCCCCACCTCAGAACCAAACACTACTGTCCTGACTGGCATGGGGCACTGGAGCA  
CCATGTTGAGGGCAAGGGCAGAGCTGGTGTCTGGGAGGGAGAAAGGTGTTGGAGGCCTTAATTATGG  
ACTGTTGGAAAAGGGTTTGTGCTCAGGACAAGGACAAGGGCAGAAAATGAGCGACTTCTGCTTCCAGAGGAAGACGAGG  
GAGCAGGAGCTTGTGACTGCTCAGAGTCTGGCTGAGGTTGACTGGGGCTGGCTCAACCCAGCAGGGGCCAGC  
GGGACCCACATCCACTGTCAGCTGGAACTTATTGTTGTTATTGAAACAGAGTTATGCT  
AACTATTGTTATAGATTGTTAATTAAAGCTTGTCTTCAAGTTCAATTGTTATTGATTCATGGTT  
GATTGTACCTCCAAAGGCCAGCTGGGATGGAGGGAGGAGAAGGGGGCTTGGGCCGCTGAGTCACATCT  
GTCCAGAGAAATTCTTGGGACTGGAGGCAAGAACGGCAGCAGGCCAGGGCTCTTCTGGAG  
GTTGGGAGGGCTTGGCCAGCCTAGGATTCTGGGTTGACTGGGGCTGGAGAGAGGGAGGAACCTCAAT  
AACCTGAAAGGGAATCCAGTTTCTGCTGGCTGGAGGGTTCTTATTGACTCTTCTGAAATGTCAGGCAG  
TGAGGTGCCCTCACTGTGAATTGTTGTTGGGGGGCTGGAGGGAGGGTGGGGGGCTGGCTCGCTCCCTCCAGC  
CTTCTGCTGCCCTGCTAACATGCCGCAACTGGGACCTCAGGGTTGCACTTCCATTCCACAGAACATGACCTGA  
TGAGGAATCTCAATAGGATGCAAAGATCAATGCAAAAATTGTTATATGAAACATATACTGGAGTCGTC  
CAAATTAAGAAAATGGACGTTAGAAGTTGCTATTAAAGCAGCTTCTAATAAAGTTGTTCAAAGCTGAAAAAA  
AA

## **FIGURE 58**

MLCLCLYVPVIGEAQTEFQYFESKGLPAELKSIFKLSVFIPSQEFSTYRQWKQKIVQAGDKDLDG  
QLDFEEFVHYLQDHEKKLRLVFKILDKKNDGRIDAQEIMQSLRDLGVKISEQQAEKILKSMDKNG  
TMTIDWNEWRDYHLLHPVENIPEIILYWKHSTIFDVGENLTVPDEFTEERQTGMWWRHLVAGGG  
AGAVSRTCTAPLDRLKVLMQVHASRSNNMGIVGGFTQMIREGGARSLWRGNGINVLKIAPESAIC  
FMAYEQIKRLVGSDQETLRIHERLVAGSLAGAIAQSSIYPMEVLKTRMALRKTGQYSGMLDCARR  
ILAREGVAAFYKGYVPNMLGIIPYAGIDLAVYETLKNAWLQHYAVNSADPGVFVLLACGTMSTC  
GQLASYPLALVRTRMQAQASIEGAPEVTMSSLFKHILRTEGAFGLYRGLAPNFMKVIPAVSISYV  
VYENLKITLGVQSR

**Important features:**

**Signal peptide:**

amino acids 1-16

**Putative transmembrane domains:**

amino acids 284-304, 339-360, 376-394

**Mitochondrial energy transfer proteins signature.**

amino acids 206-215, 300-309

**N-glycosylation sites.**

amino acids 129-133, 169-173

**Elongation Factor-hand calcium-binding protein.**

amino acids 54-73, 85-104, 121-140

## **FIGURE 59**

GGAGGCAGCGGCAGCTCCACTCAGCCAGTACCCAGATA  
CGCTGGAACCTTCCCCAGCCATGGC  
TTCCCTGGGCAGATCCTCTTCTGGAGCATAATTAGCATCATCATTATTCTGGCTGGAGCAATTG  
CACTCATCATTGGCTTGGTATTCAGGGAGACACTCCATCACAGTCACACTGTCGCCTCAGCT  
GGGAACATTGGGGAGGGATGGAATCCTGAGCTGACTTTGAACCTGACATCAAACATTCTGATAT  
CGTGATACAATGGCTGAAGGAAGGTGTTTAGGCTTGGTCCATGAGTTCAAAGAAGGCAAAGATG  
AGCTGTCGGAGCAGGATGAAATGTTCAGAGGCCGGACAGCAGTGTGCTGATCAAGTGTAGTT  
GGCAATGCCTTTGCGGCTGAAAACGTGCAACTCACAGATGCTGCCACCTACAAATGTTATAT  
CATCACTTCTAAAGGCAAGGGGAATGCTAACCTTGAGTATAAAACTGGAGCCTTCAGCATGCCGG  
AAAGTGAATGTGGACTATAATGCCAGCTCAGAGACCTTGGGTGTGAGGCTCCCGATGGTTCCCC  
CAGCCCACAGTGGCTGGGATCCCAAGTTGACCAGGGAGCCAACCTCTCGGAAGTCTCCAATAC  
CAGCTTGAGCTGAACTCTGAGAAATGTGACCATGAAGGTTGTCTGTGCTCTACAATGTTACGA  
TCAACAAACACATACTCCTGTATGATTGAAAATGACATTGCCAAAGCAACAGGGATATCAAAGTG  
ACAGAATCGGAGATCAAAGGCGGAGTCACCTACAGCTGCTAAACTCAAAGGCTCTGTGTGT  
CTCTTCTTCTTGCCATCAGCTGGCACTCTGCCTCTAGCCCTTACCTGATGCTAAAT  
GTGCCTTGGCCACAAAAAGCATGCAAAGTCATTGTTACAACAGGGATCTACAGAACTATTCAC  
CACAGATATGACCTAGTTTATATTCTGGGAGGAAATGAATTCATATCTAGAAGTCTGGAGTG  
AGCAAACAAGAGCAAGAAACAAAAAGAAGCAGAAAGCAGAAGGCTCCAATATGAACAAGATAAT  
CTATCTCAAAGACATATTAGAAGTTGGAAAATAATTCAATGTGAACTAGACAAGTGTGTTAAGA  
GTGATAAGTAAAATGCACGTGGAGACAAGTGCATCCCCAGATCTCAGGGACCTCCCCCTGCCTGT  
CACCTGGGAGTGAGAGGACAGGATAGTGCATGTTCTGTCTGAATTAGTTATATGTGC  
TGTAATGTTGCTGAGGAAGCCCTGGAAAGTCTATCCAAACATATCCACATCTTATATTCCAC  
AAATTAAAGCTGTAGTATGTACCTAACGCGCTAATTGACTGCCACTCGCAACTCAGGGCG  
GCTGCATTTAGTAATGGGTCAAATGATTCACTTTTATGATGCTTCAAAGGTGCCTGGCTTC  
TCTTCCAACTGACAAATGCCAAAGTTGAGAAAATGATCATAATTAGCATAAACAGAGCAGT  
CGGGGACACCGATTATATAAAACTGAGCACCTCTTTAAACAAAAA  
AAAAAAAAAAAAAAAAAAAAAAAAAAAAA

## **FIGURE 60**

MASLGQILFWSIISIIILAGAIALIIGFGISGRHSITVTVASAGNIGEDGILSCTFEPDIKLS  
DIVIQWLKEGVLGLVHEFKEGKDELSEQDEMFRGRTAVFADQVIVGNASLRLKNVQLTDAGTYKC  
YIITSKGKGNANLEYKTGAFSMPEVNVDYNASSETLRCEAPRWFQPTVVWASQVDQGANFSEVS  
NTSFELNSENVTMKVSVLYNVTINNTYSCMIENDIAKATGDIKVTSEIIRRSHLQLLNSKASL  
CVSSFFAISWALLPLSPYLMK

**Important features:**

**Signal peptide:**

amino acids 1-28

**Transmembrane domain:**

amino acids 258-281

**N-glycosylation sites.**

amino acids 112-116, 160-164, 190-194, 196-200, 205-209, 216-220,  
220-224

**N-myristoylation sites.**

amino acids 52-58, 126-132, 188-194

## **FIGURE 61**

TGACGTAGAACATCACCATGGCCAGCTATCCTTACCGGCAGGGCTGCCAGGAGCTGCAGGACAAG  
CACCAAGGAGGCCCTCCGGTAGCTACTACCCCTGGACCCCCAATAGTGGAGGGCAGTATGGTAGT  
GGGCTACCCCCTGGTGGTTATGGGGTCTGCCCTGGAGGGCTTATGGACCACCAGCTGG  
TGGAGGGCCCTATGGACACCCCAATCCTGGATGTTCCCTCTGGAACCTCAGGAGGACCATATG  
GCGGTGCAGCTCCCCGGGGCCCTATGGTCAGCCACCTCAAGTCTTACGGTGCCAGCAGCCT  
GGGCTTATGGACAGGGTGGCCTCCCAATGTGGATCCTGAGGCCTACTCCTGGTCCAGTC  
GGTGGACTCAGATCACAGTGGCTATATCTCCATGAAGGAGCTAAAGCAGGCCCTGGTCAACTGCA  
ATTGGTCTCATTCAATGATGAGACCTGCCATGATGATAAACATGTTGACAAGACCAAGTCA  
GGCCGCATCGATGTCTACGGCTCTCAGCCCTGTGAAATTCACTCCAGCAGTGGAAAGAACCTCTT  
CCAGCAGTATGACGGGACCGCTCGGCTCATTAGCTACACAGAGCTGCAGCAAGCTCTGCCC  
AAATGGCTACAACCTGAGCCCCAGTTACCCAGCTCTGGTCTCCCGCTACTGCCACGCTCT  
GCCAATCCTGCCATGCAGCTTGACCGCTCATCCAGGTGTGCACCCAGCTGCAGGTGCTGACAGA  
GGCCTTCCGGAGAAGGACACAGCTGTACAAGGCAACATCCGGCTCAGCTCGAGGACTTCGTCA  
CCATGACAGCTTCTCGGATGCTATGACCCAAACCATCTGTGGAGAGTGGAGTGCACCAGGGACCTT  
TCCTGGCTTCTTAGAGTGAGAGAAGTATGTGGACATCTCTTCTTCTGTCCCTCTAGAAGAAC  
ATTCTCCCTTGCTTGATGCAACACTGTTCAAAAGAGGGTGGAGAGTCCTGCATCATAGCCACCA  
AAATGTGAGGACCGGGCTGAGGCCACACAGATAGGGCCTGATGGAGGAGAGGATAGAAGTGA  
ATGTCTGATGGCCATGAGCAGTTGAGTGGCACAGCCTGGCACCAGGAGCAGGTCTTGTAAATGG  
AGTTAGTGTCCAGTCAGCTGAGCTCCACCCGTATGCCAGTGGTAGTGTTCATCGGCCTGTTACC  
GTTAGTACCTGTCTCCCTCACCAAGGCCATCCTGTCAAACGAGCCCATTCTCCAAAGTGGAAAT  
CTGACCAAGCATGAGAGAGATCTGTCTATGGGACAGTGGCTGGATTCTGCCACACCCATAAAAT  
CCTTGTGTGTTAACTCTAGCTGCCTGGGCTGGCCCTGCTCAGACAAATCTGCTCCCTGGGCAT  
CTTGGCCAGGCTCTGCCCTGCAGCTGGACCCCTCACTGCCTGCCATGCTCTGCTCGGCT  
TCAGTCTCCAGGAGACAGTGGTACCTCTCCCTGCCAATACTTTTTAATTGCAATTTC  
ATTGGGCCAAAGTCCAGTGAAATTGTAAGCTCAATAAAAGGATGAAACTCTGA

## **FIGURE 62**

MASYPYRQCPGAAGQAPGAPPGSYPGPPNSGGQYGSGLPPGGGYGGPAPGGPYGPPAGGGPYG  
HPNPGMFPSTGTPGGPYGGAAPGGPYGQPPPSSYGAQQPGLYGQGGAPPNVDPEAYSWFQSVDSDH  
SGYISMKELKQALVNCNWSSFNDETCLMMINMFDKTKSGRIDVYGFSAWKFIQWKNLFQQYDR  
DRSGSISYTELQQALSQMGYNLSPOFTQLLVSRYCPRSANPAMQLDRFIQVCTQLQLVTEAFREK  
DTAVQGNIRLSFEDFVTMTASRML

**Important features of the protein:**

**Signal peptide:**

amino acids 1-19

**N-glycosylation site.**

amino acids 147-150

**Casein kinase II phosphorylation sites.**

amino acids 135-138, 150-153, 202-205, 271-274

**N-myristoylation sites.**

amino acids 9-14, 15-20, 19-24, 33-38, 34-39, 39-44, 43-48, 61-66, 70-75, 78-83, 83-88, 87-92, 110-115

### **FIGURE 63**

## **FIGURE 64**

MQGRVAGSCAPLGLLVCLHLPGLFARSIGVVEEKVSQNFGTNLPQLGQPSSTGPSNSEHPQPAL  
DPRSNDLARVPLKLSVPPSDGFPAGGSQVRWPPSWGLPAMDSWPEDPWQMMAAAEDRLGEA  
LPEELSYLSSAAALAPGSGPLPGESSPDATGLSPEASLLHQDSESRLPRNSNLGAGGKILSQRP  
PWSLIHRVLPDHPWGTLNPSVSWGGGGPGTGWGTRPMPHPEGIWGINNQPPGTWGNINRYPGGS  
WGNINRYPGGSWGNINRYPGGSWGNIHLYPGINNPFPGVLRPPGSSWNIPAGFPNPPSPRLQWG

**Important features of the protein:**

**Signal peptide:**

amino acids 1-26

**Casein kinase II phosphorylation sites.**

amino acids 56-59, 155-158

**N-myristoylation sites.**

amino acids 48-53, 220-225, 221-226, 224-229, 247-252, 258-263,  
259-264, 269-274, 270-275, 280-285, 281-286, 305-310

## **FIGURE 65**

AAGGAGAGGCCACCGGGACTTCAGTGTCTCCTCCATCCCAGGAGCGCAGTGGCCACTATGGGTC  
TGGGCTGCCCTTGTCCCTCCTGACCCCTCTGGCAGCTCACATGGAACAGGGCCGGGTATGA  
CTTGCAACTGAAGCTGAAGGAGTCTTCTGACAAATTCCCTCATGAGTCCAGCTCCTGGAA  
TTGCTTGAAAAGCTCGCCTCCTCCATCTCCCTCAGGGACCAGCGTCACCCTCCACCATGC  
AAGATCTCAACACCATGTTGTCTGCAACACATGACCAGCCATTGAAGCCTGTGTCCTTGGCCC  
GGGCTTTGGGCCGGGATGCAGGAGGCAGGCCCGACCCCTGTCTTCAGCAGGCCCCCACCTC  
CTGAGTGGCAATAAATAAATTGGTATGCTG

## **FIGURE 66**

MGSGLPLVLLTLLGSSHGTGPGMTLQLKLKESFLTNSSYESSFLELLEKLCLLHLPSGTSVTL  
HHARSQHHVVCNT

**Important features:**

**Signal peptide:**

amino acids 1-19

**N-glycosylation site.**

amino acids 37-41

**N-myristoylation sites.**

amino acids 15-21, 19-25, 60-66

## **FIGURE 67**

ACGGACCGAGGGTTCGAGGGAGGGACACGGACCAGGAACCTGAGCTAGGTCAAAGACGCCGGC  
CAGGTGCCCGTCGCCAGGTGCCCTGGCCGGAGATGCGGTAGGAGGGCGAGCGCGAGAACCCCC  
TTCCTCGCGCTGCCAACCGCCACCCAGCCCATGGCGAACCCCGGGCTGGGCTGCTTCTGGCG  
CTGGGCCTGCCGTTCTGCTGGCCGCTGGGGCGAGCCTGGGGCAAATACAGACCACTCTGC  
AAATGAGAATAGCACTGTTGCCCTCATCCACCAGCTCCAGCTCCGATGGCAACCTGCGTCCGG  
AAGCCATCACTGCTATCATCGTGGTCTTCTCCCTTGGCTGCCTTGCTCCTGGCTGTGGGCTG  
GCACTGTTGGTGCAGCTCGGGAGAACGGCAGACGGAGGGCACCTACCGGCCAGTAGCGA  
GGAGCAGTTCTCCCATGCAGCCAGGCCCCGGGCCCCCTCAGGACTCCAAGGAGACGGTGCAGGGCT  
GCCTGCCCATTAGGTCCCTCTCCTGCATCTGTCTCCCTCATTGCTGTGACCTTGGGAAA  
GGCAGTGCCTCTCTGGGAGTCAGATCCACCCAGTGCTTAATAGCAGGGAGAAGGTACTCAA  
AGACTCTGCCCTGAGGTCAAGAGAGGATGGGCTATTCACTTTATATTTATATAAAATTAG  
TAGTGAGATGTAAAAAAAAAAAAAA

## **FIGURE 68**

MANPGLGLLLALGLPFLARWGRANGQIQTTSANENSTVLPSSSSDGTLRPEAITAIIVVFS  
LLAALLLAVGLALLVRKLREKRQTEGTYRPSSEEQFSHAAEARAPQDSKETVQGCLPI

**Important features:**

**Signal peptide:**

amino acids 1-19

**Transmembrane domain:**

amino acids 56-80

**N-glycosylation site.**

amino acids 36-40

**cAMP- and cGMP-dependent protein kinase phosphorylation site.**

amino acids 86-90

**Tyrosine kinase phosphorylation site.**

amino acids 86-94

**N-myristoylation sites.**

amino acids 7-13, 26-32

## **FIGURE 69**

GGCAGGAAATAACTAGAGAGGAACAATGGGTTATTCAAGGGTTTGTCTTCTCTAGTTCTGTGCGCTGCTGCACCAAG  
TCAAATACTCTTCAATTAAAGCTGAATAATAATGGCTTGAAGATATTGTCATTGTATAGATCCTACTGTGCGAGAA  
GATGAAAAAATAATTGAAACAATAGAGGATATTGTCAGCTACAGCTTCTACGTTGAAGGACAGACAAAAAAGA  
TTTTTTTCTAAATAATGATCTATATTAACTCCTGAGAAATATTGGAAGGAAATCTCCTAGTACACAAAGGCAAAACATGAA  
AACCATAAACATGCTGATGTTATAGTTCGACCCACTACCTCCAGGAGAGATGAAACCATACACCAAGCAGITCACA  
GAATGTGGAGAGAAAGGCGAATACATTCACTTACCCCTGACCTTCTACTTGGAAAAAAACAAATGAATATGGACCA  
CCAGGCAACTGTGTCATGAGTGGCTCACCTCCGGTGGGAGTGTGATGAGTACATGAAGATCAGCCCTTC  
TACCGTGTCAAGTCAAAAAAAATCGAAGCAACAAGGTCTCCGAGTATCTCTGAGAGAATATGAGTTATAAGTGT  
CAAGGAGGGAGCTGTCTAGTGAAGCTGCAAGATTGATTCTACACAAACATGTAATGGAAAAGATTGTCATTCTT  
CTCTGTAAGAACATACAAACAGAAAAAGCATCCTATAATTGTTATGCAAGATTGATTCTGTTGTAATTGTAACGAA  
AAACACCCATATAACAGGCTCAAGCCTACAAAACATAACTGCAATTAGAAGTACATGGGAGGTGATTAGCAAT  
TCTGAGGATTAAAAACACCATACCCATGGTACACCCACCTCCTCACCTGTCTCAATTGTAAGATCAGCTAA  
AGAATTGTCGCTTAGTTCTGATAAGTCTGGAAGCTGGGGGTAAGGACCGCCTAAATCGAATGTAACAGCAGCA  
AAACATTCTCTGCTGAGACTGTGAAATGATCTGGGGGGATGGTCACTTGTAGTACTGCCATTGTA  
AATAAGCTTAACCAATAAAAGCAGTGTGAAAGAACACATCTGAGGATTACCTATCCTGGGAGGAA  
ACTTCCATCTGCTGATTAAATATGCAATTCTAGGTGATTGGAGAGTACATTCCAACTCGATGGATCCGAAGTA  
CTGCTGCTGACTGATGGGGAGGATAACACTGCAAGTTCTGTATTGATGAGTGAAGTGAACAAAGTGGGCAATTGTTCAT  
TTTATTGCTTGGGAAGAGCTGCTGATGAGCAGTAATAGAGATGAGCAAGATAACAGGAGGAAGTCAATTGTTATGTT  
TCAGATGAAGCTCAGAACATGGCTCATTGATGCTTTGGGGCTCTTACATCAGGAAATACTGATCTCCCAAG  
TCCCTTCAGCTGCAAAGTAAGGGATTAAACTGAATAATTGCTGGATGACAGCAGTCAATTGATGTAATTGAGTACA  
GTGGGAAAGGACACGCTTCTTCTCATCACATGGAAACACTGCTCTCCAGTATTCTCTGGATCCCACTGGAACAA  
ATAATGGAAAATTCACAGTGGTGCACACTTCCAAAATGGCTATCTCAGTATTCCAGGAACCTGCAAGGTGGCACT  
TGGGCATACAATCTTCAAGCCAAGCGAACCCAGAAACATTAACACTATTACAGTAACCTCTCAGGAGCAGCAAACTTCT  
GTGCTTCAATCACAGTGAATGCTAAATGAATAAGGAGCTAACAGCTTCCCAGGCCAATGATGTTACGCAAGAA  
ATTCTACAAGGATGATGACTGTTCTGGAGGAAATGACTGCTTCTTCAATTGATCAGAAGATGACATACAAGAATT  
TTGGAACCTTGGATAATGGTGCAGGGCTGATTCTTCAAGAATGATGGAGTCACTCCAGGTTATTACAGCATAT  
ACAGAAAATGGCAGATAATGCTTAAAGTCTGGGCTCATGGAGGAGAAACACTGCCAGGCTAAATTACGCCCTCCA  
CTGAATAGACCGCGTACATACCAGGCTGGTAGTGAACGGGAAATTGAACCAAACCGGCAACGACTGAATTGAT  
GAGGAACTCAGACCCATTGGAGGATTCAAGCCAGCACATGCCAGGAGTCATTGGTATCACAGTCCCAAGC  
CTTCCCTTCTGCTGACCAATAACCCACCAAGTCATAACAGACCTTGTGACCAAGCTTGTGACATGAGGATAAGATTCTT  
ACATGGACAGCAGCAGGAGATAATTGATGTTGGGAAAGATTCAACGTTATATCATAAGAATAAGTGCAGTATTCTT  
GATCTAAGAGACAGTTTGTGATGCTCTCAAGTAATACTACTGATCTGTCACCAAGGAGGCAACTCCAAGGAA  
AGCTTGTGATTAAACCAAGAAAATATCAGAAGAAAATGCAACCCACATATTGCTTACAGGAAATATTCTGAGATGAC  
AGCAATTGACATCAAAGTATCACAATTGACCAAGTAACCTTGTGATCTGACATGAGT  
CCTCACACTCTACTCTACTCTGATGTTAAAGCTTGTGATCTGACATGAGT  
TCTGTGATTGGGCTGTTGATGTTAACTTATTAACTGACCCATTGAACTTAAACGAGAAGAAAAAAATCTC  
AAGTAGACCTAGAGAGATTTTAAACAAACAACTGTAAGTAAAGGATATTCTGATGCTTAAATTCTGAGATCTTAA  
GTGTCATGATCAAACATCATAAAATAATTGAGTGTGCGAAAGGAGATACTTGTGATTAATGAGTACATGCGATA  
TGTAAAACAGTCAAGGATTTAAATGATGCTTATTGTTGATGTTTATTGTAAGGAAATGAGTGTGAC  
ATCTCCTTCTACATGACCTGTTGATGTTAACTGACCAAGTCAACGAGGAGCAGCAATAAACACATTGGAAAA  
GAAATTAAACATCTATCTGAGTGTGACCTGTTGATGTTAACTGACCAAGTCAACGAGGAGCAGCAATAAACACATTGGAAAA  
AA

## **FIGURE 70**

MGLFRGFVFLVLCLLHQSNSTFIKLNNGFEDIVIVIDPSVPEDEKIIEQIEDMVTASTYLFE  
ATEKRFKKNVSILIPENWKENPQYKRPKHENHKHADVIVAPPTLPGRDEPYTKQFTECGEKG  
EYIHFTPDLGGKKQNEYGPPGKLFVHEWAHLRGVFDEYNEDQPFYRAKS  
KIEATRC  
SAGISGRN  
RVYKCQGGSCLSACRIDSTTKLYGKDCQFFPDKVQTEKASIMFMQS  
IDS  
V  
EFCNEKTHNQEAP  
SLQNIKCNFRSTWEVISNSEDFKNTIPMVTPPPPVFSLLKISQRIVCLVLDKSGSMGGKDRLNR  
MNQAAKHFLLQTVENG  
SWGMVHF  
DSTATIVNKLIQIKSS  
DERNTIMAGLPTYPLGGTSICSGIK  
YAFQVIGELHSQLDGSEV  
VLLTDGEDNTASSCIDEVKQSGAIVH  
FIALGRAADEAVI  
EMSKITGG  
SHFYVSDEAQNNGLIDAFGALTSGNTDLSQKSLQLESKG  
LTLNSNAWMNDTVIIDSTVGKD  
FFL  
ITWNSLPPSISLW  
DPSGTIMENFTV  
DATSKMAYLSIPG  
TAKVGTWAYNLQAKAN  
PETLTITV  
TSR  
AANSSVPPITVNA  
KMNDV  
NSF  
PS  
PMIVYAE  
ILQGYV  
PVL  
GAN  
VTA  
FIES  
QNG  
HTE  
V  
LE  
LDN  
GA  
GADS  
FKND  
GVYS  
RYFT  
AYT  
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**Signal peptide:**

amino acids 1-21

**Putative transmembrane domains:**

amino acids 284-300, 617-633

**Leucine zipper pattern.**

amino acids 469-491, 476-498

**N-glycosylation site.**

amino acids 20-24, 75-79, 340-344, 504-508, 542-546, 588-592, 628-632, 811-815, 832-836, 837-841, 852-856, 896-900

## FIGURE 71

CTCCTTAGGTGAAACCTGGGAGTAGAGTACTGACAGCAAAGACCGGAAAGACCATACGCCCCGGCAGGGTGA  
CAACAGGTGTCATTTTGTCTCGTGTGCTGCCCTCTATTCAAGGAAAGACGCCAAGGTAAATTGACCCA  
GAGGAGCAATGATGTAGGCCACCTCTAACCTCCCTTCTGAACCCCAAGTTATGCCAGGATTACTAGAGAGTGTCA  
ACTCAACCAGCAAGCGCTCCTCGGCTTAACCTGTGGTGGAGGAGAACCTTGTGGGGCTCGTTCTCTTAGCA  
GTGCTCAAGAGTGAATTGGCTGAGGGTGGACAGAAAGGAAAGGGTCCCTCTGCTGTTGGCTGCACATCAGGAA  
GGCTGTGATGGAAAGGGTAAACCTGGAGATTCACTCAGTCATTGCTCTGCTGCAAGATCATCTTAAAG  
ACTAGAGAAAGCTCTGTGTGGTTAACCTCAAGAGGCAGAACCTGTTCTAGAAGGAAATGGATGCAAGCAGCTC  
CGGGGGCCCAAACCGATGCTTCTGTGGCTAGCCAGGGAAAGCCCTCCGTGGGGCCCGCTTGAGGGATGCC  
ACCGGTTCTGGACGCGATGGCTGATTCTGAATGATGATGCTCGCCGGGGCTGCTTGTGGATTTCCGGGGTGTG  
GTTTGCTGGTGTCTCTGTGTGATCTGCTGCTGATCTGCTGACATGTGGCTGCAACCCAAAAGGTGACGAGGAGCAG  
CTGCACTGCCACGGGCAACGCCAACGGGGAGGGGGTACCCAGGCCCTCAGGAGTGGGAGGAGCAGCAC  
CGCAACTACCTGAGCACCTGAAGCAGATGCCACAGCTCAAGGAGGAGCTGCAAGGAGGAGGTGAGCAGCTCAGG  
AATGGGCACTACCAAGCAGCGATGCTGCTGGCTGGCTGGACAGGAGCCCCCAGAGAAAACCCAGGCCACCTC  
CTGGCCTCTGCACTCGCAGGGACAAGGCAGAGGTGAATGCTGGCTCAAGCTGGCACAGAGTATGAGCAGTGC  
CTTTGATAGCTTACTACAGAAAGGTGACCTGAGGACTGCCCTACCCGGGAGGGAGACCTGCTG  
AGGAAGGACAAGGGGAGTGGTGGAAAGGCAATTGAATCAGGCTTGGAGAACCTGAAACATCTGAGAGAACAGC  
CCCAATCAGGCTTACAGGCTCTGATTCTAGAAGGGATCTACCGAACAGAAAGGGACAAGGACATTTGAT  
GAGCTACCTCAAAAGGGACACAAACAGAACTCAAACGGCTCATCTTATTGACCATTCAGGCCATCATGAAA  
GTGAAAATGAAAGCTCAACATGGCAACACGCTTATCAATGTTATGCTGCTCTAGCAAAAAGGGTGGACAAGTTC  
CGGCAGTCTATGCAAGGAAATTCAAGGGAGATGTGCAITGAGCAGGGAGACTGCCATCTACTGTTGTTACTTGG  
AAAGAAGGAAATAATGAAGTCAAGGAATACTTGAAGGACTGCCAAAGCTGCAACTTCAGGAACCTTACCTTCATC  
CAGCTGAATGGGAAATTCTGGGGAAAGGGACTTGTGATGTTGGAGCCGCTTCTGGAAGGGAGCAACGCTCTC  
TTTTCTGTGATGTCAGATCTACTTCACATCTGAATTCTCAATACGTGAGGTGAATACACAGCAGGGAGAAG  
GTATTTTATCAGTTCTTCTGACTGAGTACAATCTGGCATAATATACGGCCACCATGATGCACTCCCTCCCTGGAA  
CAGCAGCTGGTATAAGAAGGAAACTGGATTGGAGAGACTTTGGATGACGTGCACTGTTGGTCAAGTTCAG  
TTCATCAATATAGGTGGTTGATGGACATCAAGGCTGGGGGGAGGGATGACCTTATGCAAGTATCTC  
CACACCAACCTCATGTTGAGCAGCTGTGCAAGGACTTTCACCTCTGGCATGAGAACGGCTGCATGGACGAG  
CTGACCCCGAGCAGTACAAGATGCACTGAGTCAAGGCTGAACAGGGCATCCACGGCAGGGCATGCTG  
GTGTTAGGACAGAGATAGGGCTACCTCGCAACAGAAACAGAAAGACAAGTAGCAAAACATGACTCCCGAGA  
GAAGGGATGTGGGAGACACTTTTCTTCTGGCAATTACTGAAAGTGGCTGCAACAGAGAAAAGACTCCATAAA  
GGACGACAAAAGAATTGGACTGATGGAGATGAGAAAGCCTGGATTCTGTGACCTTATGCAAGTATCTC  
AATCAAAATCTGGCTTGCCTGCAAAGTAACCCAGTTGCAACCTGTGAAGTGTGCAAGAACGGCAATGCTGTG  
AGATTATAAGCTTAATGGTGTGGAGTTTGTGTTACAATACACTGAGACCTGTTGTTGTGCTCATG  
AATATTGATTTAAGAGCAGTTTGTAAGGAAATTCTTAGCATGAAAGGCAAGCATATTCTCCTCATATGAATG  
GCCTATCAGCAGGGCTAGTTCTAGGAATGCTAAATATCAGAAGGAGGGAGGAGATAGGCTTATGACT  
AGTGAATGACATTAAGTAAATAATGGACAGAAAAGAAGAACCTAATGTCATATTCTCCAAAGAT  
TAACCAAAAATCTGTTATCTGGTCTCTTAACTGTCCTTTTCTTCTGTTTAAATTTAAATGCACT  
TTTTCTCTGTGAGTTATAGTCCTTAACTTACACTTGAAGCCTTACAAGAGGACAAGTGGCCTAC  
ATTTTATATTTTAAGAAGATACTTGAGATGCAATTGAGAATTTCAAGGCTCAAGGATCAATTGATGCCATAT  
CCAAGGACATGCCAAATGCTGATTCTGCTGCCACTGAATGTCAGGCATTGAGACATAGGGAGGAATGGTTGACT  
AATACAGACGTCAGACATACTTCTGTAAGAGTATTTCGAAGAGGGAGAACACTGGAGGAAAAGAAC  
ACTTCTGTTACAGAAAAGGAAACTCATTGAGCTGGTGAATCGTGTACCTAAAGTCAGAACACCACATT  
CTCCTCAGAAGTAGGGACCCCTTCTACCTGTTAAATAACCAAGTACCGTGTGAACCAAACATCTCTT  
AAAACAGGGTGCCTCTGGCTTCTGCTGCTTCCATAAGAAGAAATGGAGAAAATATATATATATATATG  
GAAAGATCAATCCATCTGCCAGAATCTAGTGGGATGGAAGTTTGTCTACATGTTATCCACCCAGGGCAGGTGG  
TAACTGAATTATTTTAAATTAAAGCAGTTCTACTCAATCAGGAGTGTGCAAGGAGGAGGAGGAGGAG  
CAAATTTTAAATAACATTAACATAGTGGTTCTTCTGTTGCTACAGTAAACTCATGTTAAAGCTCAAGAAC  
ATGCAAGCTGTTGGTGTGTTAAAGCATTGATTGATTGACTGGTAGTTATGAAATTAAACACAGG  
ATTCAAGCTGTTGGTGTGTTAAAGCATTGATTGATTGACTGGTAGTTATGAAATTAAACACAGG  
CCATGAATGGAAGGTTGATGCACAGCTAATAAATGATTGAGATGAA

## **FIGURE 72**

MMMVRRGLLAWISRVVVLLVLLCAISVLYMLACTPKGDEEQLALPRANSPTGKEGYQAVLQEWE  
EQHRNYVSSLKRQIAQLKEELQERSEQLRNGQYQASDAAGLGLDRSPPEKTQADLLAFLHSQVDK  
AEVNAGVKLATEYAAVPFDSFTLQKVYQLETGLTRHPEEKPVRKDRDELVEAIESALETLNPA  
ENSPNHRPYTASDFIEGIYRTERDKGTLYELTFKGDHKHEFKRLILFRPFSPIMKVKNEKLMAN  
TLINIVPLAKRVDKFRQFMQNPREMCIEQDGRVHLTVVYFGKEEINEVKGILENTSKAANFRNF  
TFIQLNGEFSRGKGLDVGARFWKGSNVLLFFCDVDIYFTSEFLNTCRLNTQPGKKVFYPVLFQSQY  
NPGIIYGHDAVPPLEQQQLVIKKETGFWRDFGFGMTQCQYRSDFINIGGF DLDIKGWGGEDVHLYR  
KYLHSNLIVV RTPVRLFHLWHEKRCMDELTPEQYKMCMSKAMNEASHGQLGMLVFRHEIEAHL  
RKQKQKTSSKKT

**Important features:**

**Signal peptide:**

amino acids 1-27

**N-glycosylation sites.**

amino acids 315-319, 324-328

**N-myristylation sites.**

amino acids 96-102, 136-142, 212-218, 311-317, 339-345, 393-399

**Amidation site.**

amino acids 377-381

## **FIGURE 73**

GAGACTGCAGAGGGAGATAAAGAGAGAGGGCAAAGAGGCAGCAAGAGATTGTCCTGGGATCCA  
GAAACCCATGATACCCACTGAAACACCGAATCCCTGGAAGGCCACAGAGACAGACAGCAAGA  
GAAGCAGAGATAAAACACTCACGCCAGGAGCTCGCTCGCTCTCTCTCTCACTCC  
CCTCCCTCTCTGCTGTCTAGTCCTAGTCCTAAATTCCAGTCCCCCTGCACCCCTTC  
CTGGGACACTATGTTCTCCGCCCTCCTGCTGGAGGTATTGGATCCTGGCTGCAGATGGGG  
GTCAACACTGGACGTATGAGGCCACATGGTCAGGACCATGGCCAGCCTTACCCGTAGTGT  
GGAAACATGCCAGCGATATTCAAGACAGACAGTGTGACATTGACCCGTGATTGCC  
TGCTCTGCAGCCCCACGGATATGACCAGCCTGGCACCGAGCCTTGGACCTGCACAACAATGCC  
ACACAGTGCAACTCTCTGCCCTTACCCGTATCTGGTGGACTTCCCAGAAATATGTAGCT  
GCCAGCTCACCTGCACTGGGTCAAGAAAGGATCCCCAGGGGGTCAGAACACCAAGATCACAG  
TGAAGCCACATTGCAAGAGCTCCACATTGTACATTGACTCTGATTCTATGACAGCTTGAGTG  
AGGCTGCTGAGAGGCCTCAGGCCCTGGCTGTCTGGCATCCTAATTGAGGTGGTGAGACTAAG  
AATATAGCTTATGAACACATTGAGTCATTGCATGAAGTCAGGCATAAAGATCAGAACACCTC  
AGTCCTCCCTCAACCTAACAGAGAGCTGCCCTCAGCTCCCCAACAGCTGGGCAGTACTCCGCTACAATG  
GCTCGCTCACAACTCCCCCTGCTACCAGAGTGTGCTCTGGACAGTTTTATAGAAGGTCCAG  
ATTTCAATGGAACAGCTGAAAAGCTTCAGGGACATTGTTCTCACAGAACAGGAGCCCTCTAA  
GCTTCTGGTACAGAACTACCGAGCCCTCAGCTCTCAATCAGCGCATGGCTTGCTTCTTCA  
TCCAAGCAGGATCCTCGTATACCACAGGTGAAATGCTGAGTCTAGGTGAGGAATCTGGTGGC  
TGTCTCTGCCTTCCTGGCTGTTATTCATTGCTAGAAAGATTGGAAGAACAGGCTGGAAAA  
CCGAAAGAGTGTGGCTTCACCTCAGCACAAGCCACGACTGAGGCATAAATTCTCTCAGATAC  
CATGGATGTGGATGACTTCCCTCATGCCATCAGGAAGCCTCTAAATGGGTGAGGATCTGG  
CCAGAAACACTGTAGGAGTAGTAAGCAGATGTCCTCCCTGGACATCTCTAGAGAGGAAT  
GGACCCAGGCTGTCATTCCAGGAAGAACTGCAGAGCCTCAGCCTCTCCAAACATGTAGGAGGA  
ATGAGGAAATCGCTGTGTTGTTAATGCAGAGANAAACTCTGTTAGTTGCAAGGGAAAGTTGG  
ATATACCCCAAAGCTCTACCCCTCACTTTATGCCCTTCCCTAGATATACTGCGGGATCT  
CTCCTAGGATAAAGAGTTGCTGTTGAAGTTGATATTTGATCAATATATTGAAATTAAG  
TTTCTGACTTT

## **FIGURE 74**

MLFSALLLEVIWILAADGGQHWTYEGPHQDHWPASYPECGNNAQSPIDIQTDSVTFPDPDLPALQ  
PHGYDQPGTEPLDLHNNNGHTVQLSLPSTLYLGGGLPRKVAAQLHLHWGQKGSPPGSEHQINSEAT  
FAELHIVHYDSDSYDSLSEAAERPQGLAVLGILIEVGETKNIAYEHILSHLHEVRHKDQKTSVPP  
FNLRELLPKQLGQYFRYNGSLTPPCYQSVLWTVFYRRSQISMEQLEKLQGTLFSTEEEPSKLLV  
QNYRALQPLNQRMVFASFIQAGSSYTTGEMLSLGVGILVGCLCLLLAVYFIARKIRKKRLENRKS  
VVFTSAQATTEA

**Important features of the protein:**

**Signal peptide:**

amino acids 1-15

**Transmembrane domain:**

amino acids 291-310

**N-glycosylation site.**

amino acids 213-216

**Eukaryotic-type carbonic anhydrases proteins**

amino acids 197-245, 104-140, 22-69

## **FIGURE 75**

TGCCGCTGCCGCCGTGCTGCTGTTGCTCCCTGGCGGCCCTGGGACGGGCAGTCCCTGTGTC  
TCTGGTGGTTGCCTAACCTGCAAACATCACCTTCTATCCATCAACATGAAGAATGTCCTACA  
ATGGACTCCACCAGAGGGTCTCAAGGAGTTAAAGTTACTTACACTGTGCAGTATTCATCACAA  
ATTGGGCCACCAGAGGTGGCACTGACTACAGATGAGAAGTCCATTCTGTTGTCCTGACAGCTCC  
AGAGAAGTGGAAAGAGAAATCCAGAAGACCTTCCTGTTCCATGCAACAAATATACTCCAATCTGA  
AGTATAACGTGTCGTGTTGAATACTAAATCAAACAGAACGTGGTCCAGTGTGACCAACCAC  
ACGCTGGTGCTCACCTGGCTGGAGCCGAACACTTTACTGCGTACACGTGGAGTCCTCGTCCC  
AGGGCCCCCTGCCGTGCTCAGCCTCTGAGAACAGCAGTGTGCCAGGACTTTGAAAGATCAATCAT  
CAGAGTTCAAGGCTAAATCATCTCTGGTATGTTGCCATATCTATTACCGTGTGTTCTTT  
TCTGTGATGGCTATTCCATCTACCGATATATCCACGTTGGCAAAGAGAAACACCCAGCAAATT  
GATTTGATTTATGAAATGAATTGACAAAAGATTCTTGTGCCTGCTGAAAAAAATCGTGATTA  
ACTTTATCACCTCAATATCTGGATGATTCTAAAATTCTCATCAGGATATGAGTTACTGGGA  
AAAAGCAGTGTATCCAGCCTTAATGATCCTCAGCCAGCGGGAACCTGAGGCCCCCTCAGGA  
GGAAGAGGAGGTGAAACATTAGGTATGCTCGCATTGATGAAATTGGTGAACCTGAG  
AAAACACGGAAGGTACTTCTCACCCAGCAAGAGTCCTCAGCAGAACAAACCCCCGGATAAA  
ACAGTCATTGAATATGAATATGATGTCAGAACCAACTGACATTGCGGGGCCCTGAAGAGCAGGA  
GCTCAGTTGCAGGAGGGAGGTGTCCACACAAGGAACATTATTGGAGTCGCAGGCAGCGTTGGCAG  
TCTTGGGCCCGAAACGTTACAGTACTCATACACCCCTCAGCTCCAAGACTTAGACCCCCCTGGC  
CAGGAGCACACAGACTCGGAGGAGGGCCGGAGGAAGAGCCATCGACGACCCCTGGCGACTGGGA  
TCCCCAAACTGGCAGGCTGTGATTCCCTCGCTGTCCAGCTCGACCAGGATTAGAGGGCTGCG  
AGCCTCTGAGGGGGATGGGCTCGGAGAGGGTCTCTATCTAGACTCTATGAGGAGCCGGCT  
CCAGACAGGCCACCAGGAGAAAATGAAACCTATCTCATGCAATTCTATGGAGGAATGGGGTTATA  
TGTGCAGATGGAAAACTGATGCAACACTCCCTTGCCTTTGTTCTGTGCAAACAAAGTGAG  
TCACCCCTTGATCCCAGCCATAAGTACCTGGGATGAAAGAAGTTTTCCAGTTGTCACTGT  
CTGTGAGAATTACTTATTCTTCTATTCTCATAGCAGCTGTGATTGGTTCATGCATGTA  
GGTCTCTAACAAATGATGGTGGCAGACTGGGTGCAGAATTATTAGGTGGGTGT  
AGCAGTCATAAAATGTTGCCAGACTGGGTGCAGAATTATTAGGTGGGTGT

## **FIGURE 76**

MSYNGLHQRFKELKLLTLCISIQGPPEVALTTDEKSISVVLTAPEKWKRNPEDLPVSMQQIY  
SNLKYNVSLNTKSNRTWSQCVTNHTLVLTWLEPNLTYCVHVESFVPGPPRRAQPSEKQCARTLK  
DQSSEFKAKIIFWYVLPISITVFLFSVMGYSIYRYIHVGKEKHPANLILYGNFDFKRFVPAEK  
IVINFITLNISDDSKISHQDMSLLGKSSDVSSLNDPQPSGNLRPPQEEEVKGHLGYASHLMEIFC  
DSEENTEGTSLTQQESLSRTIPPDKTVIEYEDVRTTDICAGPEEQLSILQEEVSTQGTLLESQA  
ALAVLGPQLQSYTPQLQDLDPLAQEHTDSEEGPEEEPSTTLVDWDPQTGRLCIPSLSFDQDS  
EGCEPSEGDSLGEGLSRLYEEPAPDRPGENETYLMQFMEEWGLYVQMN

**Important features:**

**Signal peptide:**

amino acids 1-28

**Transmembrane domain:**

amino acids 140-163

**N-glycosylation sites.**

amino acids 71-74, 80-83, 89-92, 204-207, 423-426

## **FIGURE 77**

GAGGAGCGGGCCGAGGACTCCAGCGTGCCAGGTCTGGCATCCTGCACTTGCTGCCCTCTGACAC  
CTGGGAAG**ATGGCCGGCCCGTGGACCTTCACCCCTCTCTGTGGTTGCTGGCAGCCACCTTGATC**  
CAAGCCACCCCTCAGTCCCCTGAGTTCTCATCCTCGGCCAAAAGTCATCAAAGAAAAGCTGAC  
ACAGGAGCTGAAGGACCACAACGCCACCAGCATCCTGCAGCAGCTGCCGCTGCTCAGTGCCATGC  
GGGAAAAGCCAGCCGGAGGCATCCCTGTGCTGGGAGCCTGGTGAACACCGTCCCTGAAGCACATC  
ATCTGGCTGAAGGTCAAGATCCCCCTGGACATGGTGGCTGGATTCAACACGCCCTGGTCAAGACCA  
GGAGCTGCTAGTCAAGATCCCCCTGGACATGGTGGCTGGATTCAACACGCCCTGGTCAAGACCA  
TCGTGGAGTTCCACATGACGACTGAGGCCAAGGCCACCATCCGCATGGACACCCAGTGAAGTGGC  
CCCACCCGCCCTGGTCCCTCAGTGA**CTGTGCCACCAGCCATGGGAGCCTGCGCATCCAACTGCTGTA**  
TAAGCTCTCCTTCCTGGTGAACGCCCTAGCTAAGCAGGTCAAGCAGGTCAACCTCCTAGTGCCATCCTGC  
CCAATCTAGTGAAAAACCAGCTGTGCTCCCGTATCGAGGCTTCATGGCATGTATGCAGAC  
CTCCTGCAGCTGGTGAAGGTGCCATTCCCTCAGCATTGACCGTCTGGAGTTGACCTCTGTA  
TCCTGCCATCAAGGGTGAACCAAGCATTCAAGCTGAGCTGCTCCCTGACAATGCCACCCTGGACAACATCCCG  
AGGTGACCAAGTGGTCAATAACTCTGCAGCTTCCCTGACAATGCCACCCTGGACAACATCCCG  
TTCAGCCTCATCGTGAGTCAGGACGTGGTGAAGCTGCAGTGGCTGCTGTGCTCTCCAGAAGA  
ATTCAATGGTCCCTGGTGA**ACTCTGTGCTCCCTGAGAGTGCCATGGCTGAAGTCAAGCATCGGGC**  
TGATCAATGAAAAGGCTGCAGATAAGCTGGATCTACCCAGATCGAAGATCTAACTCAGGAC  
ACTCCCGAGTTTTTATAGACCAAGGCCATGCCAAGGTGCCCAACTGATCGTGTGGAAAGTGT  
TCCCTCCAGTGAAGGCCCTCCGCCTTGTTCAACCCTGGCATCGAAGCCAGCTGGAAAGCTCAGT  
TTTACACCAAGGTGACCAACTTATACTCAACTTGAATAACATCAGCTCTGATCGGATCCAGCTG  
ATGAACACTGGGATTGGCTGGTCCAACCTGATGTTCTGAAAAACATCATCACTGAGATCATCCA  
CTCCATCCTGCTGCCGAACCAGAAATGGCAAATTAAAGATCTGGGTCCCTGAGTGTCAATTGGTGAAGG  
CCTTGGGATTGAGGCACTGAGTCCTCACTGACCAAGGATGCCCTGTGCTTACTCCAGCCTCC  
TTGTGAAACCCAGCTCTCTGTCTCCAGT**GAAGACTTGGATGCCAGCCATCAGGAAGGCTGG**  
GTCCCAGCTGGGAGTATGGGTGTGAGCTATAGACCATCCCTCTGCAATCAATAAACACTTG  
CCTGTGAAAAA

## **FIGURE 78**

MAGPWTFTLLCGLLAATLIQATLSPTAVLILGPKVIKEKLTQELKDHNATSILQQPLLSAMREK  
PAGGIPLVLSLVNTVLKHI IWLKVITANIILQLQVKPSANDQELLVKIPLDMVAGFNTPLVKTIVE  
FHMTTEAQATIRMDTSASGPTRLVLSDCATSHGSLRIQLLYKLSFLVNALAKQVMNLLVPSLPNL  
VKNQLCPVIEASFNGMYADLLQLVKVPISLSIDRLEFDLLYPAIKGDTIQLYLGAKLLDSQGKVT  
KWFNNSAASLTMPPTLDNIPFSLIVSQDVVKAAVAAVLSPEEFMVLLDSVLPESAHLKSSIGLIN  
EKAADKLGSTQIVKILTQDTPEFFIDQGHAKVAQLIVLEVFPSSEALRPLFTLGIEASSEAQFYT  
KGDQLILNLNNISSLRQIQLMNSGIGWFQPDVLKNIITEIIHSILLPNQNGKLRSGVPVSLVKALG  
FEAAESSLTKDALVLTPASLWKPSSPVSQ

**Important features of the protein:**

**Signal peptide:**

amino acids 1-21

**N-glycosylation sites.**

amino acids 48-51, 264-267, 401-404

**Glycosaminoglycan attachment site.**

amino acids 412-415

**LBP / BPI / CETP family proteins.**

amino acids 407-457

## **FIGURE 79**

GAGAGAAGTCAGCCTGGCAGAGAGACTCTGAAATGAGGGATTAGAGGTGTTCAAGGAGCAAGAGC  
TTCAGCCTGAAGACAAGGGAGCAGTCCTGAAGACGCTCTACTGAGAGGTCTGCCATGGCCTCT  
CTTGGCCTCCAACTGTGGGCTACATCTAGGCCTCTGGGCTTTGGGCACACTGGTGCCAT  
GCTGCTCCCAGCTGGAAAACAAGTTCTATGTCGGTGCCAGCATTGTGACAGCAGTTGGCTTCT  
CCAAGGGCCTCTGGATGGAATGTGCCACACACAGCACAGGCATCACCCAGTGTGACATCTATAGC  
ACCCCTCTGGCCTGCCCGCTGACATCCAGGCTGCCAGGCCATGATGGTGACATCCAGTGAAT  
CTCCTCCCTGGCCTGCATTATCTCTGTGGTGGGATGAGATGACAGTCTTCTGCCAGGAATCCC  
GAGCCAAAGACAGAGTGGCGGTAGCAGGTGGAGTCTTTCATCCTGGAGGCCTCTGGGATTC  
ATTCCCTGTGCTGGAATCTCATGGGATCCTACGGGACTCTACTCACCACGGTGCCTGACAG  
CATGAAATTGAGATTGGAGAGGCTTTACTTGGGATTATTCCTCCCTGTCTCCCTGATAG  
CTGGAATCCTCATCCTGCTTTCTGCTCATCCCAGAGAAATCGCTCCAACACTACGATGCTAC  
CAAGCCAACCTCTGCCACAAGGAGCTCCAAGGCCTGGTCAACCTCCAAAGTCAAGAGTGA  
GTTCAATTCTACAGCCTGACAGGTATGTGTAAGAACCAGGGGCCAGAGCTGGGGGTGGCTG  
GGTCTGTAAAAACAGTGGACAGCACCCCGAGGGCCACAGGTGAGGGACACTACCACGGATCGT  
GTCAGAGGTGCTGAGGATAGACTGACTTGGCATTGGATTGAGCAAAGGCAGAAATGGG  
GCTAGTGTAAACAGCATGCAGGTTGAATTGCCAAGGGATGCTGCCATGCCAGCCTTCTGTTCC  
TCACCTTGCTGCTCCCTGCCCTAAGCCCCAACCTCAACTGAAACCCATTCCCTAACCCA  
GGACTCAGAGGATCCCTTGCCCTCTGGTTACCTGGACTCCATCCCCAACCCACTAACATACA  
TCCCACGTGACTGACCCCTGTGATCAAAGACCCCTCTCTGGCTGAGGTTGGCTTAGCTCATT  
GCTGGGGATGGAGAGAAGCAGTGGTTGTGGGCTATTGCTCTAACCTACTTCTAACGCTC  
CCTCCAAAGAAACTGATTGCCCTGGAACCTCCATCCACTCTTGTATGACTCCACAGTGTCCA  
GACTAATTGTGCATGAAATAAAACCATCCTACGGTATCCAGGGAACAGAAAGCAGGATG  
CAGGATGGAGGACAGGAAGGCAGCCTGGGACATTAAAAAAATA

## **FIGURE 8o**

MASLGLQLVGYILGLLGLLGTIVAMLLPSWKTSSYVGASIVTAVGFSKGLWMECATHSTGITQCD  
IYSTLLGLPADIQAAQAMMVTSAAISLACIISVVGMRCTVFCQESRAKDRVAVAGGVFFILGGL  
LGFIPVAWNLHGILRDFYSPLVPSMKFEIGEALYLGISSLFSLIAGIILCFSCSSQRNRSNY  
DAYQAQPLATRSSPRPGQPPKVSEFNSYSLTGYV

**Important features of the protein:**

**Signal peptide:**

amino acids 1-24

**Transmembrane domains:**

amino acids 82-102, 117-140, 163-182

**N-glycosylation site.**

amino acids 190-193

**PMP-22 / EMP / MP20 family proteins.**

amino acids 46-59

## **FIGURE 81**

CCACACGCGTCCGCGCCTCTCCCTCTGCTGGACCTTCCTCGTCTCCATCTCTCCCTCCTTC  
CCCGCGTTCTCTTCCACCTTCTTCTTCCACCTTAGACCTCCCTCCCTGCCCTCCTTCCT  
GCCACCGCTGCTTCCCTGGCCCTCTCGACCCCGCTCTAGCAGCAGACCTCCTGGGTCTGTGG  
GTTGATCTGTGGCCCTGTGCCTCCGTGTCCTTCGTCTCCCTCCCTCCGACTCCGCTCCGG  
ACCAGCGGCTGACCCCTGGGAAAGGAGGGTTCCCGAGGGTGAGGGTCCCTCCCTTGCTGGGA  
CTCGCGTCTGGTTCCCCCTGGACTCCCACGCTCGAGCCGCCAGACATGTTCTGCCTTT  
CCATGGGAAGAGATACTCCCCCGCGAGAGCTGGCACCCCTACTTGGAGCCACAAGGCCTGATGT  
ACTGCCTGCGCTGTACCTGCTCAGAGGGCCCATGTGAGTTACCGCCTCCACTGTCCGCCT  
GTCCACTGCCCCAGCCTGTGACGGGCCACAGCAATGCTGTCCCAAGTGTGGAACCTCACAC  
TCCCTCTGGACTCCGGGCCCCACCAAAGTCTGCCAGCACAAACGGGACCATGTACCAACACGGAG  
AGATCTCAGTCCCCATGAGCTGTTCCCTCCCGCCTGCCAACCAAGTGTGTCCTCTGCAGCTGC  
ACAGAGGGCCAGATCTACTGCGGCCTCACAAACCTGCCCCGAACCAGGCTGCCAGCACCCCTCCC  
ACTGCCAGACTCCTGCTGCCAAGCCTGCAAAGATGAGGCAAGTGAGCAATCGGATGAAGAGGACA  
GTGTGCAGTCGCTCATGGGTGAGACATCCTCAGGATCCATGTTCCAGTGTGATGCTGGGAGAAAG  
AGAGGGCCGGCACCCAGCCCCACTGGCTCAGGCCCTCTGAGCTTCCATCCCTGCCACTT  
CAGACCCAAGGGAGCAGGCAGCACAACTGTCAAGATCGCCTGAAGGAGAAACATAAGAAAGCCT  
GTGTGCATGGCGGAAGACGTACTCCCACGGGAGGTGTGGCACCCGGCTTCCGTGCCCTCGC  
CCCTGCCCTGCATCCTATGCACCTGTGAGGATGGCCGCCAGGACTGCCAGCGTGTGACCTGTCC  
CACCGAGTACCCCTGCCGTACCCCGAGAAAGTGGCTGGGAAGTGTGCAAGATTGCCAGAGG  
ACAAAGCAGACCCGGCCACAGTGAGATCAGTCAACCTGCTGAGGACTGCCAGGGCCGGTC  
CTCGTCCACACATCGGTATCCCAAGGCCAGACAACCTGCGTCGCTTGCCCTGGAACACGAGGC  
CTCGGACTTGGTGGAGATCTACCTCTGGAAGCTGGTAAAGATGAGGAAACTGAGGCTCAGAGAG  
GTGAAGTACCTGGCCAAGGCCACACAGCAGAACATCTCCACTTGACTCAGATCAAGAAAGTCAG  
GAAGCAAGACTTCCAGAAAGAGGCACAGCACTCCGACTGCTCGCTGGCCCCACGAAGGTCACT  
GGAACGTCTCCAGGCCAGACCCCTGGAGCTGAAGGTACGCCAGTCCAGACAAAGTGACCAAG  
ACATAACAAAGACTAAACAGTTGCAGATATGAGCTGTATAATTGTTATTATATTAATAA  
TAAGAAGTTGCATTACCCCTCAAAAAAAAAAAAAAAAAAAAAA

## **FIGURE 82**

MVPEVRVLSSLLGLALLWFPLDSHARARPDMFCLFHGKRYSPGESWHPYLEPQGLMYCLRCTCSE  
GAHVSCYRLHCPPVHCPQPVTEPQQCCPKCVEPHTPSGLRAPPKSCQHNGTMYQHGEIFSAHELP  
PSRLPNQCVLCSCTEGQIYCGLTTCPPEPGCPAPLPLPDSCCQACKDEASEQSDEEDSVQSLHGVR  
HPQDPCSSDAGRKRGPGTPAPTGLSAPLSFIPRHFRPKGAGSTTVKIVLKEKHKKACVHGGKTY  
HGEVWHPAFRAFGPLPCILCTCEDGRQDCQRVTCPTEYPCRHPEKVAGKCKICPEDKADPGHSE  
ISSTRCPKAPGRVLVHTSVSPSPDNLRRFALEHEASDLVEIYLWKLVKDEETEAQRGEVPGPRPH  
SQNLPLDSDQESQEARNLPERGTLPTARWPPRRSLERLPSPDGAEGHGQSRQSDQDITKT

**Signal peptide:**

amino acids 1-25

## **FIGURE 83**

GACAGCTGTCTCGATGGAGTAGACTCTCAGAACAGCGCAGTTGCCCTCCGCTCACCGCAGAGCCTCTCC  
GTGGCTTCCGCACCTTGAGCATTAGGCCAGTTCCCTCTCTCTAATCCATCCGTACCTCTCCGTCA  
TCCGTTCCATGCCGTGAGGTCACAGAACACATCCATGGCTCTCATGCTCAGTTGGTCTGAGTC  
TCCTCAAGCTGGATCAGGGCAGTGGCAGGTGTTGGCCAGACAAGCCTGTCCAGGCCTGGTGGGGAG  
GACGCAGCATTCTCTGTTCCCTCTAAGACCAATGCAGAGGCCATGGAAGTGCCTTCTCAGGGG  
CCAGTTCTCTAGCGTGGTCCACCTCTACAGGGACGGGAAGGACCCAGCATTATGCAGATGCCACAGTATC  
AAGGCAGGACAAAATGGTGAAGGATTCTATTGCGGAGGGCGCATCTCTGAGGCTGGAAAACATTACT  
GTGTTGGATGCTGGCTCTATGGTGCAGGATTAGTCCCAGTCCTACTACAGAACGCCATCTGGAGCT  
ACAGGGTGCAGCACTGGGCTCAGTCCCTCTCATTCACAGGGATATGTTGATAGAGACATCCAGCTAC  
TCTGTCAGTCCTCGGCTGGTCCCCGGCCACAGCGAAGTGGAAAGGTCACAAGGACAGGATTGTC  
ACAGACTCCAGGACAAACAGAGACATGCATGGCCTGTTGATGTTGAGATCTCTGACCGTCAAGAGAA  
CGCCGGGAGCATATCCTGTTCCATGCGGATGCTCATCTGAGCCGAGAGGTTGAATCCAGGGTACAGATAG  
GAGATACCTTTTCGAGCCTATATCGTGGCACCTGGCTACCAAAGTACTGGAAACTCTGCTGTGGCTA  
TTTTTGGCATTGTTGACTGAAGATTTCTCTCCAAATTCCAGTGGAAATCCAGGCCAACTGGACTG  
GAGAAGAAAAGCACGGACAGGCAGAATTGAGAGACGCCGAAACACGCAAGTGGAGGTGACTCTGGATCCAG  
AGACGGCTACCCGAAGCTCGCTTCTGATCTGAAAACGTAAACCCATAGAAAAGCTCCCCAGGGAGGTG  
CCTCACTCTGAGAAGAGATTACAAGGAAGAGTGTGGTGGCTCTCAGAGTTCCAAGCAGGGAAACATTA  
CTGGGAGGTGGACGGAGGACACAATAAAAGGTGGCGCTGGAGTGTGGCTGGATGATGTGGACAGGAGGA  
AGGAGTACGTGACTTTGCTCCCGATCATGGTACTGGTCTCAGACTGAATGGAGAACATTGTATTTC  
ACATTAATCCCCGTTTATCAGCGTCTTCCCCAGGACCCACCTACAAAATAGGGTCTTCTGACTA  
TGAGTGTGGACCCTCTCTCAACATAATGACCAGTCCCTATTATACCCATGACATGTCGTTG  
AAGGCTTATTGAGGCCATCTCTCTGAGTATCGCTCTATAATGAGCAAATGGAACCTCCATAGTCATCTGC  
CCAGTCACCCAGGAATCAGAGAAAGAGGCCCTTGGCAAAGGGCTCTGCAATCCAGAGACAAGAACAG  
TGAGTCCTCCTCACAGGCAACCACGCCCTCCCTCCCCAGGGTGAATGTAGGATGAATCACATCCACAT  
TCTTCTTAGGGATATTAGGTCTCTCTCCAGATCCAAAGTCCCGCAGCAGGCCAAAGGTGGCTTCCA  
GATGAAGGGGACTGGCTGTCCACATGGAGTCAGGTGTCAGGCTGCCCTGAGCTGGAGGGAAAGAAGG  
CTGACATTACATTAGTTGCTCTCACTCCATCTGCTAAAGTGTGATCTGAAATACCACCTCTCAGGTGAAG  
AACCGTCAGGAATTCCCATCTCACAGGCTGTGGTGTAGATTAGTAGACAAGGAATGTGAATAATGCTTAG  
ATCTTATTGATGACAGAGTGTATCTAATGGTTGTCATTATATTACACTTCAGTAAAAAA

## **FIGURE 84**

MALMLSVLSSLKLGSQWQVFGPDKPVQALVGEDAASFCLSPKTNAEAMEVRRFRGQFSSVH  
LYRDGKDQPQMOPQYQGRTKLVKDSIAEGRISLRLENITVLDAGLYGCRISSQSYYQKAIWELQ  
VSALGSVPPLISITGYVDRDIQLLCQSSGWFPRPTAKWKGPGQQLSTDSTNRDMHGLFDVEISL  
TVQENAGSISCSMRHAHLSREVESRVQIGDTFFEPISWHLATKVLGILCCGLFFGIVGLKIFFSK  
FQWKIQAELDWRRKHGQAEELRDARKHAVEVTLDPETAHPKLCVSDLKTVTHRKAQEVPHSEKRF  
TRKSVVVASQSFQAGKHYWEVDGGHNRWRGVCRDDVDRRKEYVTLSPDHGYWVRLNGEHYFT  
LNPRFISVFPRTPPTKIGVFLDYECGTISFFNINDQSLIYTLTCRFEGLLRPYIEYPSYNEQNGT  
PIVICPVTQESEKEASWQRASAIPETSNSESSSQATTPFLPRGEM

**Signal peptide:**

amino acids 1-17

**Transmembrane domain:**

amino acids 239-255

## **FIGURE 85**

AACAGACGTTCCCTCGGGCCCTGGCACCTCTAACCCAGACATGCTGCTGCTGCTGCTGCCCT  
GCTCTGGGGGAGGGAGAGGGCGAAGGACAGACAAGTAAACTGCTGACGATGCAGAGTTCCGTGA  
CGGTGCAGGAAGGCCTGTGTCCATGTGCCCTGCTCCTCTCTACCCCTCGCATGGCTGGATT  
TACCTGGCCCAGTAGTCATGGCTACTGGTCCGGAAAGGGCAATACAGACCAGGATGGTCC  
AGTGGCCACAAACAACCCAGCTGGCAGTGTGGAGGACTCGGGACCGATTCCACCTCCTG  
GGGACCCACATACCAAGAATTGCACCCCTGAGCATCAGAGATGCCAGAAGAAGTGATGCGGGAGA  
TACTTCTTCGTATGGAGAAAGGAAGTATAAAATGGATTATAAACATCACCGGCTCTGTGAA  
TGTGACAGCCTTGACCCACAGGCCAACATCCTCATCCCAGGCACCCCTGGAGTCCGGCTGCC  
AGAATCTGACCTGCTCTGTGCCCTGGGCCTGTGAGCAGGGACACCCCTATGATCTCCTGGATA  
GGGACCTCCGTGTCCCCCTGGACCCCTCACCCGGCTCCTCGTGCTCACCCATCCCACA  
GCCCCAGGACCATGGCACCAGCCTCACCTGTCAGGTGACCTCCCTGGGCCAGCGTGACCAGA  
ACAAGACCGTCCATCTAACGTGTCCTACCCGCTCAGAACTGTGACCATGACTGTCTCCAAGGA  
GACGGCACAGTATCCACAGTCTGGAAATGGCTATCTGTCACTCCAGAGGGCCAGTCT  
GCGCCTGGTCTGTGCAGTGTGACAGTGCAGTTGACAGCAATCCCGCTGCCAGGCTGAGCCTGAGCTGGA  
GAGGCCTGACCCCTGTGCCCTCACAGCCCTAAACCCGGGGTGCGGGCTGCCTTGGGTGCAC  
CTGAGGGATGCAGCTGATTCACCTGCAGAGCTCAGGGAGTGACTCAGGGGGTGGTGGGGAGCTGGAG  
GAACGTCTCCCTGCAGAGCAAGCCACATCAGGGAGTGACTCAGGGGGTGGTGGGGAGCTGGAG  
CCACAGCCCTGGTCTCTGTCCCTGCGTCATCTCGTTTGTAGGTGAGGTCTGCAGGAAGAAA  
TCGGCAAGGCCAGCAGCGGGCGTGGAGATACGGGCATAGAGGGATGCAACCGCTGTCAGGGGTTC  
AGCCTCTCAGGGGCCCTGTCAACCTGGGCAAGACAGCTCCCCCAGGCCCTCCCCCA  
CTTCTGCCCGCTCCTCAGTGGGGAGGGAGGTCCAGGTTATGCATCCCTCAGCTCCAGATGGTGA  
AAGCCTGGGACTCGGGGGACAGGGGGCCACTGACCCGAGGTACTCGAGATCAAGATCCACAG  
ATGAAAACTGCAGAGACTCACCCTGATTGAGGGATCAGGCCCTCCAGGGCAAGGGGAAGGTCA  
GAGGGTGATTCTTGAGAATTAACAGCCCTCAACGTGATGAGGTTATGATAACACTATGATTTATG  
TGCAGAGGTGAAAAGCACACGGCTTTAGAGGTCAAAAGGTTATCTCAACACGTGTGCCC  
TCCCTTTTATTTTTTAACAAAGACAAAATCCCTTA

## **FIGURE 86**

MLLLLLPLLWGRERAEGQTSKLLTMQSSVTQEGLCVHVPCFSYPSHGWIYPGPVVHGYWFREG  
ANTDQDAPVATNNPARAVWEETRDRFHLLGDPHTKNCTLSIRDARRSDAGRYFFRMEKGSIKWNY  
KHHRLSVNVNTALTHRPNILIPGTLESGCPQNLTCSPWACEQGT~~PPM~~ISWIGTSVSPLDPSTTRS  
SVLTLIPQ~~P~~QD~~H~~GTS~~L~~T~~C~~QVTFPGASVTTNKT~~V~~HLN~~V~~SYPPQNLMTVFQGDGT~~V~~STVLGN~~G~~SSL  
SLPEGQSLRLVCAVD~~A~~DSNPPARLSLSWRGLTLCPSQPSNPGVLELPWVHLRDAAEFTCRAQNP  
LGSQQVYLN~~V~~SLQSKATSGVTQGVVGGAGATALVFLSFCVIFVVVRSCRKKSARPAAGVGDTGIE  
DANAVRG~~S~~ASQGPLTEPWAEDSPPDQPPPASARSSVGEGELOYASLSFQMVKPWDSRGQEA~~T~~DE  
YSEIKIHR

**Signal peptide:**

amino acids 1-15

**Transmembrane domain:**

amino acids 351-370

## **FIGURE 87**

AGAAAGCTGCACTCTGTTGAGCTCCAGGGCGCAGTGGAGGGAGGTGAAGGAGCTCTGTAC  
CCAAGGAAAGTGCAGCTGAGACTCAGACAAGATTACAATGAACCAACTCAGCTCCTGCTGTTTC  
TCATAGCGACCACCAGAGGATGGAGTACAGATGAGGCTAATACTTACTTCAGGAATGGACCTGT  
TCTTCGTCATCTCTGCCAGAAGCTGCAAGGAAATCAAAGACGAATGTCCTAGTGCATTGA  
TGGCCTGTATTTCTCCGCACTGAGAATGGTTATCTACCAAGACCTCTGTGACATGACCTCTG  
GGGGTGGCGGCTGGACCCCTGGTGGCCAGCGTGCATGAGAATGACATGCGTGGAGTGCACGGTG  
GGCGATCGCTGGTCAGTCAGCAGGGCAGCAAAGCAGACTACCCAGAGGGGACGGCAACTGGGC  
CAACTACAACACCTTGGATCTGCAGAGGCCACGAGCGATGACTACAAGAACCTGGCTACT  
ACGACATCCAGGCCAAGGACCTGGCATCTGGCACGTGCCAATAAGTCCCCATGCAGCACTGG  
AGAAACAGCTCCCTGCTGAGGTACCGCACGGACACTGGCTCCTCCAGACACTGGACATAATCT  
GTTTGGCATCTACCAGAAATATCCAGTGAAATATGGAGAAGGAAAGTGTGACTGACAACGGCC  
CGGTGATCCCTGTGGCTATGATTTGGCACGCCAGAAAACAGCATCTTATTACTCACCTAT  
GGCCAGCGGAATTCACTGCGGGATTGTCAGTTCAAGGTATTTAATAACGAGAGAGCAGCCAA  
CGCCTTGTGTGGATGAGGTACCGCACGGATGTAACACTGAGCATCACTGCATTGGTGGAGGAG  
GATACTTCCAGAGGCCAGTCCCAGCAGTGTGGAGATTTCTGGTTTGATTGGAGTGGATAT  
GGAACACTCATGTTGGTACAGCAGCAGCCGTGAGATAACTGAGGCAGCTGTGCTTCTATTCTATCG  
TTGAGAGTTTGTGGAGGGAACCCAGACCTCTCCCAACCATGAGATCCAAAGGATGGAGAA  
CAACTTACCCAGTAGCTAGAATGTTAATGGCAGAAGAGAAAACAATAATCATATTGACTCAAGA  
AAAAAA

## **FIGURE 88**

MNQLSFLFLIATTRGWSTDEANTYFKEWTCSSSPSLPRSCKEIKDECPSAFDGLYFLRTENGVI  
YQTFCDMTSGGGGWTLVASVHENDMRGKCTVGDRSSQQGSKADYPEGDGNWANYNTFGSAEAAT  
SDDYKNPGYYDIQAKDLGIWHVPNPKSPMQHWRNSSLRYRTDTGFLQTLGHNLFGIYQKYPVKYG  
EGKCWTNDGPVIPVYDFGDAQKTASYYSPYQREFTAGFVQFRVFNNERAANALCAGMRVTGCN  
TEHHCIGGGYFPEASPQQCGDFSGFDWSGYGTHVGYSSREITEAAVLLFYR

**Important features:**

**Signal peptide:**

amino acids 1-16

**N-glycosylation site.**

amino acids 163-167

**Glycosaminoglycan attachment sites.**

amino acids 74-78, 289-293

**N-myristoylation sites.**

amino acids 76-82, 115-121, 124-130, 253-259, 292-298

## **FIGURE 8q**

CTAGATTGTCGGCTTGC~~GGGG~~AGACTTCAGGAGTCGCTGTCTGAAC~~TCCAGCCTCAGAGAC~~  
CGCCGCCCTTGT~~CCCC~~GAGGGCATGGGCGGGTCTCAGGGCTTGTGCCCTCTCGCTTCTGACG  
CTCCTGGCGCATCTGGTGGTCGTACACCTTATTCTGGT~~CCC~~GGGACAGCAACATACAGGCCTG  
CCTGCCTCTCACGTTACCCCCGAGGAGTATGACAAGCAGGACATT~~CAGCTGGTGGCCGCGCT~~  
CTGTCACCC~~TGGG~~CTCTTGAGTGGAGCTGGCCGGTTCC~~T~~TCAGGAGTCTCCATGTTAAC  
AGCACCCAGAGCCTCATCTCCATTGGGCTCACTGTAGTGCATCCGTGGCC~~CTG~~CC~~T~~TCAT  
ATT~~CGAGC~~GTTGGGAGTGC~~ACT~~ACGTATTGGTACATTTTG~~T~~CTGCAGTGCC~~CT~~CCAGCTG  
TC~~ACT~~GAAATGGCTTATT~~CGT~~CACCGT~~TT~~GGGCTGAAAAAGAAAC~~CC~~TTCTGATTAC~~CT~~CA  
TGACGGGAAC~~CTA~~AGGACGAAGCCTACAGGGCAAGGGCCG~~CT~~CGTATT~~CC~~TGGAAAGAAGGAAG  
GCATAGGCT~~CGT~~TTCC~~CC~~CTGGAAACTG~~CT~~CTGCTGGAGGATATGTGTTGGAAATAATTACG  
TCTTGAGTCTGGGATTATCCGATTGTATTAGT~~G~~CTTGTAATAAAATATGTTTG~~T~~AGTAACA  
TTAAGACTTATATA~~CAG~~TTAGGGACAATTAAAAAAAAAAA

## **FIGURE 90**

MGRVSGLVPNSRFLTLLAHLVVVITLFWRSRDSNIQACLPLTFTPEEYDKQDIQLVAALSVTGLFA  
VELAGFLSGVSMFNSTQSLISIGAHCSASVALSFFIFERWECTTYWYIFVFCSALPAVTEMALFV  
TVFGLKKKP

Transmembrane domain:

amino acids 12-28 (type II), 51-66, 107-124

## **FIGURE 91**

CTGGGACCCGAAAAGAGAAGGGGAGAGCGAGGGACGAGAGCGGAGGAGGAAGATGCAACTGAC  
TCGCTGCTGCTCGTGTCTGGTGCAGGGTAGCCTATCTGGTATCTGTGCCAGGATGATG  
GTCCTCCGGCTCAGAGGACCTGAGCGTATGACCACGAGGGCAGCCCCGGCCGGTGCCT  
CGGAAGCGGGGCCACATCTCACCTAACGCTCCGCCCCATGGCAATTCCACTCTCCTAGGGCTGCT  
GGCCCCGCTGGGAGGCTTGGGCATTCTGGCAGCCCCCAACCGCCGAACCACAGCCCC  
CACCCCTAGCCAAGGTGAAGAAAATCTTGGCTGGGCGACTTCTACTCCAACATCAAGACGGTG  
GCCCTGAACCTGCTCGTCACAGGGAAAGATTGTGGACCATGGCAATGGACCTCAGCGTCCACTT  
CCAACACAATGCCACAGGCCAGGGAAACATCTCCATCAGCCTCGTCCCCCAGTAAAGCTGTAG  
AGTTCCACCAAGGAACAGCAGATCTCATCGAAGCCAAGGCCTCCAAAATCTCAACTGCCGATG  
GAGTGGGAGAAGGTAGAACGGGCCGCCGACCTCGCTTGACCCACGACCCAGCCAAGATCTG  
CTCCCGAGACCACGCTCAGAGCTCAGCCACCTGGAGCTGCTCCAGCCCTCAAAGTCGTCTGTG  
TCTACATCGCCTTCTACAGCACGGACTATCGGCTGGTCCAGAAGGTGTGCCAGATTACAAC  
CATAGTGATAACCCCTACTACCCATCTGGGTGACCCGGGCAGGCCACAGAGGCCAGGCCAGGGC  
TGGAAAGGACAGGCCCTGCCCATGCAGGAGACCATCTGGACACCAGGGCAGGGAAAGGGTTGGCCTC  
AGGCAGGGAGGGGGGTGGAGACGAGGAGATGCCAAGTGGGCCAGGGCAAGTCTCAAGTGGCAG  
AGAAAAGGGTCCCAAGTGCTGGTCCCAACCTGAAGCTGTGGAGTGACTAGATCACAGGAGCACTGG  
AGGAGGAGTGGCTCTGTGCAGCCTCACAGGGCTTGCCACGGAGCCACAGAGAGATGCTGG  
TCCCCGAGGCCCTGTGGCAGGGCAGTCAGTGTGGCCCCAGATCAAGTCATGGGAGGAAGCTAAGC  
CCTTGGTTCTGCCATCCTGAGGAAGATAGCAACAGGGAGGGGAGATTTCATCAGTGTGGACA  
GCCTGTCAACTTAGGATGGATGGCTGAGAGGGCTTCCCTAGGAGCCAGTCAGCAGGGTGGGTGG  
GCCAGAGGAGCTCCAGCCCTGCCCTAGTGGGCCCTGAGCCCCCTGTGTGCTGAGCATGG  
CATGAGGCTGAAGTGGCAACCTGGGTCTTGATGTCTTGACAGATTGACCATCTGTCTCAGC  
CAGGCCACCCCTTCCAAAATCCCTCTCTGCCAGTACTCCCCCTGTACCAACCCATTGCTGATG  
GCACACCCATCCTTAAGCTAACAGCAGGAGATTGTGGCCTCCACACTAACGGCCACAGGCCATC  
CGCGTGTGTGTGCTCCCTTCCACCCCAACCCCTGCTGGCTCCTCTGGAGCATCCATGTCCCG  
GAGAGGGGTCCCTAACAGTCAGCCTCACCTGTCAGACCGGGGTTCTCCGGATCTGGATGGCGC  
CGCCCTCTCAGCAGCGGGCACGGGTGGGGCGGGCCGGCCAGAGCATGTGCTGGATCTGTC  
TGTGTGTCTGTGTGGTGGGGAGGGAGGGAAAGTCTGTGAAACCGCTGATTGCTGACTTT  
TGTGTGAAGAATCGTGTCTGGAGCAGGAAATAAGCTGCCCGGGCA

## **FIGURE 92**

MQLTRCCFVFLVQGSILVICGQDDGPPGSEDPERDDHEGQPRPRVPRKRGHISPKSRPMA  
NSTLGLLAPPGEAWGILGQPPNRPNHSPPPSAKVKKIFGWGDFYSNIKTVANLLVTGKIVDHGN  
TFSVHFQHNATGQGNISISLVPPSKAVEFHQQQIFIEAKASKIFNCRMEWEKVERGRRTSLCTHDP  
AKICSRDHAQSSATWSCSQPKVVCVYIAFYSTDYRLVQKVCVDNYHSDTPYPSG

**Important features of the protein:**

**Signal peptide:**

amino acids 1-14

**N-glycosylation sites.**

amino acids 62-65, 127-130, 137-140, 143-146

**2-oxo acid dehydrogenases acyltransferase**

amino acids 61-71

### **FIGURE 93**

CGGTGGCCATGACTGCGGCCGTGTTCTCGGCTGCGCCTCATTGCCTCGGGCCTGCGCTCGCC  
CTTTATGTCTCACCATGCCATCGAGCCGTTGCGTATCATCTTCCTCATGCCGGAGCTTCTT  
CTGGTTGGTGTCTACTGATTGTCGCCCTGTTGGTTCATGGCAAGAGTCATTATTGACAACA  
AAGATGGACCAACACAGAAATATCTGCTGATCTTGGAGCGTTGTCTGTCTATATCCAAGAA  
ATGTTCCGATTGCATATTATAAACTCTTAAAAAAAGCCAGTGAAGGTTGAAGAGTATAAACCC  
AGGTGAGACAGCACCCCTCTATGCGACTGCTGGCCTATGTTCTGGCTTGGCTTGGATCATGA  
GTGGAGTATTTCCCTTGTGAATACCCCTATCTGACTCCTGGGCCAGGCACAGTGGGCATTCT  
GGAGATTCTCCTCAATTCTCCTTATTCACTGCTGGTCATTATCTGCTGCATGT  
ATTCTGGGCATTGTATTTTGATGGCTGTGAGAAGAAAAAGTGGGCATCCTCTTATCGTC  
TCCTGACCCACCTGCTGGTGTCAAGCCAGACCTTCATAAGTTCTTATTATGAAATAAACCTGGCG  
TCAGCATTATAATCCTGGTGTCACTGGCACCTGGCATTCTAGCTGCGGGAGGCAGCTGCCG  
AAGCCTGAAACTCTGCCTGCTGCCAAGACAAGAACTTCTTACAACCAGCGCTCCAGAT  
AACCTCAGGGAACCAGCACTTCCAAACCGCAGACTACATCTTAGAGGAAGCACAACGTGCCT  
TTTCTGAAAATCCCTTTCTGGTGAATTGAGAAAGAAATAAAACTATGCAGATA

## **FIGURE 94**

MTAAVFFGCAFIAGPALALYVFTIAIEPLRIIFLIAGAFFWLVSLLISSLVWFMARVIIDNKDG  
PTQKYLLIFGAFVSVYIQEMFRFAYYKLLKASEGLKSINPGETAPSMRLLAYVSGLGFGIMSGV  
FSFVNTLSDSLGP GTVGIHGDSPQFFLYSAFMTLVIIILLHVFWGIVFFDGCEKKKGILLIVLLT  
HLLVSAQTFISSYYGINLASAFIILVLMGTWAAGGSCRSLKLCLLCQDKNFLLYNQSR

**Important features of the protein:**

**Signal peptide:**

amino acids 1-19

**Transmembrane domains:**

amino acids 32-51, 119-138, 152-169, 216-235

**Glycosaminoglycan attachment site.**

amino acids 120-123

**Sodium:neurotransmitter symporter family protein**

amino acids 31-65

## **FIGURE 95**

AATTTTCACCAGAGTAAACTTGAGAAACCAACTGGACCTTGAGTATTGTACATTTGCCTCGTG  
GACCCAAAGGTAGCAATCTGAAACATGAGGAGTACGATTCTACTGTTTGCTCTAGGATCAAC  
TCGGTCATTACCACAGCTAAACCTGTTGGACTCCCTCCCACAAAACTGGCTCCGGATCAGG  
GAACACTACCAAAACCAACAGCAGTCAAATCAGGTCTTCCTTAAAGTCTGATACCATTAACA  
CAGATGCTCACACTGGGCCAGATCTGCATCTGTTAAATCCTGCTGCAGGAATGACACCTGGTAC  
CCAGACCCACCCATTGACCCCTGGGAGGGTTGAATGTACAACAGCAACTGCACCCACATGTGTTAC  
CAATTTTGTCACACAACTTGGAGCCCAGGGCACTATCCTAAGCTCAGAGGAATTGCCACAAATC  
TTCACGAGCCTCATCATCCATTCTGTTCCCGGGAGGCATCCTGCCACCAGTCAGGCAGGGC  
TAATCCAGATGTCCAGGATGGAAGCCTCCAGCAGGAGGAGCAGGTGTAATCTGCCACCCAGG  
GAACCCCAGCAGGCCCTCCCAACTCCCAGTGGCACAGATGACGACTTGCAGTGACCACCCCT  
GCAGGCATCCAAAGGAGCACACATGCCATCAGGAAGCCACCACAGAAATCAGCAAATGGAATTCA  
GTAAGCTGTTCAAATTTCAACTAAGCTGCCCGAATTGGTGATACATGTGAATCTTATC  
ATTGATTATATTATGGAATAGATTGAGACACATTGGATAGTCTTAGAAGAAATTAAATTCTTAATT  
TACCTGAAAATATTCTGAAATTCAAGAAAATATGTTCTATGTAGAGAAATCCAACTTTAAAAAA  
CAATAATTCAATGGATAAAATCTGTCTTGAATATAACATTATGCTGCCTGGATGATATGCATAT  
TAAAACATATTGGAAAAACTGGAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAA  
AAAAAAAAAAAAAAAAAAAAAAAAAAAAAA

## **FIGURE 96**

MRSTILLFCLLGSTRSLPQLKPALGLPPTKLAPDQGTLPNQQQSNQVFPSSLILPTQM  
LTLPDLHLLNPAAGMTPGTQTHPLTLGGLNVQQQLHPHVLPIFVTQLGAQGTILSSEE  
LPQIFTSLIIHSLFPGGILPTSQAGANPDVQDGSLPAGGAGVNPATQGTPAGRLPTPSG  
TDDDFAVTTPAGIQRSTHAIIEATTESANGIQ

**Signal peptide:**

amino acids 1-16

## **FIGURE 97**

## **FIGURE 98**

MVPAWLWLLCVSVPQALPKAQPAELSVEVPENYGGNFPLYLTKLPLPREGAEGQIVLSDGSKAT  
EGPFAMDPDSGFLLVTRALDREEQAEYQLQVTLEMQDGHVLWGPQPVLVHVKDENDQVPHFSQAI  
YRARLSRGTRPGIPFLFLEASDRDEPGTANSDLRFHILSQAPAQPSPDMFQLEPRLGALALSPKG  
STS LDHALERTYQLLVQVKDMGDQASGHQATATVEVS IESTWVSLEPIH LAENLKVLYPHHMAQ  
VHWSGGDVHYHLESHPPGPFEVNAEGNLYVTRELDREAQAEYLLQVRAQNSHGEDYAAPLELHVL  
VMDENDNVPICPPRDPVT S IPELSPPGTEVTRLSAEDADAPGSPNSHVYQLLSPEPEDGVEGRA  
FQVDPTSGSVTLGVPLRAGQNILLVLAMDLAGAEGGFSTCEVEAVTDINDHAPEFITSQIG  
PISLPEDVEPGTLVAMLTAIDADLEPAFRIMDFAIERGDTEGT FGLDWEPDSGHVRLRLCKNLSY  
EAAPSHEVVVVVQSVAKLVGPGPGPAGATATVTLVERVMPPPQLDQESYEASVPISAPAGSFLLT  
IQPSDPISRTLRFSLVNDSEGWL CIEKFSGEVHTAQSLQGAQPGDTYTVLVEAQDTALTTLAPVPS  
QYLCTPRQDHGLIVSGPSKDPDLASGHGPYSFTLGPNPTVQRDWRLQTLNGSHAYLTLALHWVEP  
REHIIPVVVSHNAQM WQLLVRVIVCRCNVEGQCMRKVGRMKGMPTKLSAVGILVGTLVAIGIFLI  
LIFTHWTMSRKKDQPADSVPLKATV

**Signal peptide:**

amino acids 1-18

**Transmembrane domain:**

amino acids 762-784

## **FIGURE 99**

GGCTGACCGTGCTACATTGCTGGAGGAAGGCTAAGGAACCCAGGCATCCAGCTGCCACGCC  
AGTCCAAGATTCTTCCCAGGAACACAAACGTTAGGAGACCCACGCTCTGGAAAGCACCAGCCTTA  
TCTCTCACCTTCAAGTCCCCTTCTCAAGAACTCTGTCTTGTCTTGCCTCTAAAGTCTGGTAC  
ATCTAGGACCCAGGCATCTTGCTTCCAGCCACAAAGAGACAGATGAAGATGCAGAAAGGAAATG  
TTCTCCTTATGTTGGTCTACTATTGCAATTAGAAGCTGCAACAAATTCAATGAGACTAGCACC  
TCTGCCAACACTGGATCCAGTGTGATCTCAGTGGAGCCAGCACAGCCACCAACTCTGGGTCAG  
TGTGACTCCAGTGGGTCAAGCACAGCCACCATCTCAGGGTCCAGCGTGCACCTCCAATGGGTC  
GCATAGTCACCAACTCTGAGTCCATACAACCTCCAGTGGGATCAGCACAGCCACCAACTCTGAG  
TTCAGCACAGCGTCCAGTGGGATCAGCATAGCCACCAACTCTGAGTCCAGCACAACCTCCAGTGG  
GGCCAGCACAGCCACCAACTCTGAGTCCAGCACACCCCTCAGTGGGCCAGCACAGTCACCAACT  
CTGGGTCAGTGTGACCTCAGTGGAGCCAGCAGTGCACCAACTCTGAGTCCAGCACAGTGTCC  
AGTAGGGCCAGCAGTGCACCAACTCTGAGTCTAGCACACTCTCAGTGGGCCAGCACAGCC  
CAACTCTGACTCCAGCACAACCTCCAGTGGGCTAGCACAGCCACCAACTCTGAGTCCAGCACA  
CCTCCAGTGGGCCAGCACAGCCACCAACTCTGAGTCCAGCACAGCCACAGTGTCCAGTAGGGCCAGCA  
GCCACCAACTCTGAGTCCAGCACACCTCCAGTGGGCCAGCACAGCCACCAACTCTGAGTCC  
AACGACCTCAATGGGCTGGCACAGCCACCAACTCTGAGTCCAGCACAGCCACCTCCAGTGGGCC  
GCACAGCCACCAACTCTGACTCCAGCAGTGTCCAGTGGGCCAGCAGTGCACCAACTCTGAG  
TCCAGCACGACCTCCAGTGGGCCAGCACAGCCACCAACTCTGAGTCCAGCACGACCTCCAGTGG  
GGCTAGCACAGCCACCAACTCTGACTCCAGCACAACCTCCAGTGGGCCAGCACAGCCACCAACT  
CTGAGTCCAGCACAGTGTCCAGTGGGATCAGCACAGTCACCAATTCTGAGTCCAGCACACCC  
AGTGGGCCACACAGCCACCAACTCTGAGTCCAGTACGACCTCCAGTGGGCCACACAGCC  
CAACTCTGAGTCCAGCAGTGTCCAGTGGGCCAGCACAGCCACCAACTCTGAGTCCAGCACA  
CCTCCAGTGGGTCAAGCACAGCCACCAACTCTGAGTCCAGCACACCCCTCCAGTGGGCC  
GCCACCAACTCTGACTCCAGCACAACCTCCAGTGGGCCAGCACAGCCACCAACTCTGAGTCTAG  
CACAGTGTCCAGTGGGATCAGCACAGTCACCAATTCTGAGTCCAGCACACCC  
ACACAGCCACCAACTCTGGGTCCAGTGTGACCTCTGCAAGCTCTGGAACAGCAGCTCTGACTGGA  
ATGCACACAACCTCCCATAGTCATCTACTCGAGTGAAGTGGGAAAGCCTGGGGCTCTTGCTGG  
GCCGTGGAAATCTCCTCATCACCCCTGGTCTCGGTTGTGGCGCCGTGGGGCTCTTGCTGG  
TCTTCTCTGTGAGAAACAGCCTGGTCCAGGCCCTGGAGAAACACCTTAACACAGCTGTCTACCAC  
CATGGCTCAACCATGGCCTGGTCCAGGCCCTGGAGAAATCATGGAGCCCCACAGGCC  
GTGGAGTCTTAACCTGGTCTGGAGGAGACCAAGTATCATCGATAGCCATGGAGATGAGCGGGAG  
ACAGCGGGCCTGAGCAGCCCCGGAGCAAGTGCCTGAGTCAAGTGGCTTACAGGAAGGAAGAGAC  
CCCCAGACCTGGTTCTCATCCAGGAGACCCCTCCAGCTTGTGAGATCTGAA  
AATCTTGAAGAAGGTAACTCCTACCTTCTGCTTACAGACACTGGAAAGAGAAACTATAT  
TGCTCATTTAGCTAAGAATAAACATCTCATCTAACACACAGACAAAGAGAAAGCTGTGCTTG  
CCCCGGGTGGGTATCTAGCTGAGATGAACCTCAGTTATAGGAGAAAACCTCCATGCTGGACTC  
CATCTGGCATCAAAATCTCACAGTAAATCCAAAGACCTCAAAAAAAAAAAAAAAA  
AAAAAAAAAAAAAAAAAAAAAAA

## **FIGURE 100**

MKMQGNVLLMFGLLLHLEATNSNETSTSANTGSSVISSGASTATNGSSVTSSGVSTATISGS  
SVTSNGVSIVTNSEFHTTSSGISTATNSEFSTASSGISIATNSESSTTSSGASTATNSESSTPSS  
GASTVTNGSSVTSSGASTATNSESSTVSSRASTATNSESSTLSSGASTATNDSSTTSSGASTA  
TNSESSTTSSGASTATNSESSTVSSRASTATNSESSTTSSGASTATNSESRTTSNGAGTATNSES  
STTSSGASTATNDSSTVSSGASTATNSESSTTSSGASTATNSESSTTSSGASTATNDSSTTSS  
GAGTATNSESSTVSSGISTVTNSESSTPSSGANTATNSESSTTSSGANTATNSESSTVSSGASTA  
TNSESSTTSSGVSTATNSESSTTSSGASTATNDSSTSSEASTATNSESSTVSSGISTVTNSES  
STTSSGANTATNGSSVTSAGSGTAALTGMHTTSHSASTAVSEAKPGGSLVPWEIFLITLVSVVA  
AVGLFAGLFFCVRNLSLRNTFNTAVYHPHGLNHGLGPGPGENHGAPHRPRWSPNWFWRPVS  
AMEMSGRNSGP

**Signal peptide:**

amino acids 1-20

**Transmembrane domain:**

amino acids 510-532

## **FIGURE 101**

GGCCGGACGCCTCCCGTTACGGGATGAATTAACGGCGGTTCCGCACGGAGGTTGTGACCCCTA  
CGGAGCCCCAGCTTGCCCACGCACCCCACTCGGCCTCGCGCGTGCCTGCTGTACAGGTG  
GGAGGCTGGAACATATCAGGCTGAAAAACAGAGTGGGTACTCTCTGGGAAGCTGGCAACAAAT  
GGATGATGTGATATATGCATTCCAGGGGAAGGGAAATTGTGGTGCTCTGAACCCATGGTCAATT  
AACGAGGCAGTTCTAGCTACTGCACGTACTTCATAAAGCAGGACTCTAAAGCTTGGAAATCAT  
GGTGTCAATGGAAAGGGATTTACTTATACTGACTCTGTTGGGAAGCTTTGGAAAGCATT  
TCATGCTGAGTCCCTTTTACCTTGATGTTGATAACCCATCTGGTATCGCTGGATCAACAAAC  
CGCCTTGTGGCAACATGGCTCACCTACCTGTGGCATTATTGGAGACCATGTTGGTGTAAAAGT  
GATTATAACTGGGATGCATTGTCCTGGAGAAAGAAGTGTCAATTATCATGAACCATCGGACAA  
GAATGGACTGGATGTTCTGTGGAATTGCTGATGCGATATAGCTACCTCAGATTGGAGAAAATT  
TGCCTCAAAGCGAGTCTCAAAGGTGTTGGATTGGTGGCCATGCGAGCTGCTGCCTATAT  
CTTCATTCAAGGAAATGGAAGGATGACAAGAGCATTGAGACATGATTGATTACTTTGTG  
ATATTCAACCACTTCACCTCCATATTCCAGAAGGGACTGATCTCACAGAAAACAGCAAG  
TCTCGAAGTAATGCAATTGCTGAAAAAAATGGACTTCAGAAAATGAATATGTTTACATCCAAG  
AACTACAGGCTTACTTGTGGTAGACCGTCAAGAGAAGGTAAGAACCTTGATGCTGTCCATG  
ATATCACTGTGGCGTATCCTCACAAACATTCCCAATCAGAGAAGCACCTCCTCCAAGGAGACTT  
CCCAGGGAAATCCACTTCACGTCCACCGGTATCCAATAGACACCCCTCCCCACATCCAAGGAGGA  
CCTTCAACTCTGGTGCACAAACGGTGGGAAGAGAAAGAAGAGGAGCTGCCTTCTATCAAG  
GGGAGAAGAATTTTATTTACCGGACAGAGTGTCAATTCCACCTTGCAAGTCTGAACCTAGGGTC  
CTTGTGGTCAAATTGCTCTATACTGTATTGGACCCCTGTTAGCCCTGCAATGTGCCTACTCAT  
ATATTGTACAGTCTGTTAAGTGGTATTATAATCACCATTGTAATCTTGCTGCAAGAGA  
GAATATTGGTGGACTGGAGATCATAGAACCTGCAATTGACTTACACAAACAGCCACAT  
TTAAATTCAAAGAAAATGAGTAAGATTATAAGTTGCCATGTGAAAACCTAGAGCATATTG  
GAAATGTTCTAAACCTTCTAAGCTCAGATGCATTGCACTGACTATGTCGAATATTCTACT  
GCCATCATTATTGTTAAAGATATTGCACTTAATTGCTGGGAAAATATTGCTACAATT  
TTAATCTCTGAATGTAATTGATACTGTGACATAGCAGGGAGTGATGGGGTGAATAACTT  
GGGCCAGAATATTAAACAAATCATCAGGCTTTAAA

## **FIGURE 102**

MHSRGREIVVLLNPWSINEAVSSYCTYFIKQDSKSFGIMVSWKGIYFILTLFWGSFFGSIFMLSP  
FLPLMFVNPSWYRWINNRLVATWLTPVALLETMFGVKVIITGDAFVPGERSVIIMNHRTRMDWM  
FLWNCLMRYSYLRLEKICLKAISLKGVPFGFWAMQAAAYIFIHRKWKDDKSHFEDMIDYFCDIHEP  
LQLLIFPEGTDLTENSRSNAFAEKNGLQKYEYVLHPRTTGTFVVDRLREGKNLDAVHDITVA  
YPHNIPQSEKHLLQGDFPREIHFHVRYPIDTLPTSKEDLQLWCHKRWEEKERLRSFYQGEKNF  
YFTGQSVIPPCKSELRLVVKLLSILYWTLFSPAMCLLIYLYSLVKWYFIITIVIFVLQERIFGG  
LEIIELACYRLLHKQPHLNSKKNE

**Important features of the protein:**

**Signal peptide:**

amino acids 1-22

**Transmembrane domains:**

amino acids 44-63, 90-108, 354-377

## **FIGURE 103**

CGGCTCGAGCGGCTCGAGTGAAGAGCCTCCACGGCTCTGCGCCTGAGACAGCTGGCCTGACC  
TCCAAATCATCCATCCACCCCTGCTGTCATCTGTTCTAGTTCTACGAGCTGGTGTCAAGGACAGTGGCAAGT  
TCCATGGCTTTGTCATTTGGTTCTCAGTTCTACGAGCTGGTGTCAAGGACAGTGGCAAGT  
CACTGGACCGGGCAAGTTGTCAGGGCTTGGTGGGGAGGACGCCGTGTCAGGACAGTGGCAAGT  
TTCCTGAGACCAGTGCAGAGGCTATGGAAGTGCAGGTTCTCAGGAATCAGTTCCATGCTGTGGTC  
CACCTCTACAGAGATGGGAAGACTGGGAATCTAACGAGATGCCACAGTATCGAGGGAGAACTGA  
GTTTGTGAAGGACTCATTGCAAGGGGGCGTGTCTCTAAGGCTAAAAAACATCACTCCCTCGG  
ACATCGCCTGTATGGGTGTCAGTCCCAGATTACGATGAGGAGGCCACCTGGGAGCTG  
CGGGTGGCAGCACTGGGCTCACTTCCCTCATTTCCATCGTGGGATATGTTGACGGAGGTATCCA  
GTTACTCTGCCTGCCTCAGGGCTGGTCCCCCAGCCCACAGCCAAGTGGAAAGGTCCACAAGGAC  
AGGATTGTCAGACTCCAGAGCAAATGCAGATGGGTACAGCCTGTATGATGTTGGAGATCTCC  
ATTATAGTCCAGGAAAATGCTGGGAGCATATTGTTCCATCCACCTTGTGACGAGACTCATGA  
GGTGGAAATCCAAGGTATTGATAGGAGAGACGTTTCCAGCCCTCACCTTGGCCCTGGCTTCTA  
TTTACTCGGGTTACTCTGTTGCCCCCTGTGTGGTGTATGGGATGATAATTGTTCTC  
AAATCCAAAGGAAAATCCAGGGCAACTGGACTGGAGAAGAAAGCACGGACAGGCAGAATTGAG  
AGACGCCCGAAACACGCACTGGGAGGTGACTCTGGATCCAGAGACGGCTACCCGAAGCTCGC  
TTTCTGATCTGAAAATCTGAAACCCATAGAAAAGCTCCCAGGAGGTGCTCACTCTGAGAAGAGA  
TTTACAAGGAAGAGTGTGGTGGCTTCAGGGTTCCAAGCAGGGAGACATTACTGGGAGGTGGA  
CGTGGGACAAAATGTAGGGTGGTATGTTGGAGTGTGTCGGGATGACGTAGACAGGGGGAAAGAAC  
ATGTGACTTGTCTCCAACATGGGATTTGGGCTCTAGACTGACAACAGAACATTGTATTTC  
ACATTCAATCCCCATTATCAGCCTCCCCCAGCACCCCTCTCACAGAGTAGGGGCTTCT  
GGACTATGAGGGTGGGACCATCTCTTCAATAACAAATGACCAGTCCCTTATTATACCTGC  
TGACATGTCAGTTGAAGGCTGTTGAGACCTATACTCCAGCATGGATGTATGACGGAGAAAAG  
GGGACTCCCATTCTCATATGTCAGTGTCTGGGATGAGACAGAGAACCCCTGCTAAAGGGC  
CCCACACCAAGACCCAGCACAGCCAAGGGAGATGCTCCCGACAGGTGGCCCCAGCTTCTCT  
CCGGAGCCTGCGCACAGAGTCAAGCCCCACTCTCTTCTAGGGAGCTGAGGTTCTGTGCCC  
TGAGCCCTGCAAGCGGCAGTCACAGCTTCCAGATGAGGGGGATTGGCCTGACCCCTGTGGAG  
TCAGAAGCATGGCTGCCCTGAAGTGGGACGGAATAGACTCACATTAGGTTAGTTGTGAAAA  
CTCCATCCAGTAAAGCAGTCTGAACAAGTCACAACCTCCCAGGCTCCTCATTTGCTAGTCACGG  
ACAGTGAATTCTGCTCACAGGTGAAGATAAAGAGACAACGAATGTGAATCATGCTTGAGGTT  
TGAGGGACAGTGTGCTAATGATGTTTATATTACATTTCACCCATAACTCTGTT  
TGCTTATTCCACATTAATTACTTTCTCTATACCAAATCACCCATGGAATAGTTATTGAAACACC  
TGCTTGTGAGGCTCAAAGAATAAAGAGGAGGTAGGATTTCACTGATTCTATAAGCCCAGCAT  
TACCTGATACCAAAACCAAGGCAAAGAAAACAGAAGAAGAGGAAGGAAAACACAGGTCCATATCC  
CTCATTAACACAGACACAAAAATTCTAAATAAAATTTAACAAATTAAACTAAACAATATATTAA  
AAGATGATATATAACTACTCAGTGTGGTTGTCCCACAAATGCAGAGTTGGTTAATATTAAAT  
ATCAACCCAGTGTAAATTCAAGCACATTAATAAGTAAAAAGAAAACCATAAAAAAAAAAAAAA

## **FIGURE 104**

MAFVLILVLSFYELVSGQWQVTGPGKVFQALVGEDAVFSCSLFPETSAEAMEVRRFRNQFHAVVH  
LYRDGEDWESKQMPQYRGRTEFKKDSIAGGRVSLRLKNITPSDIGLYGCWFSSQIYDEEATWELR  
VAALGSLPLISIVGYVDGGIQLLCLLSGWFPQPTAKWKGPGQGDLSSDSRANADGYSLYDVEISI  
IVQENAGSILCSIHLAEQSHEVESKVLIGETFFQPSPWRLASILLGLLCGALCGVVMGMIIVFFK  
SKGKIQAEQELDWRKKHGQAEELRDARKHAVEVTLDPETAHPKLCVSDLKTVTHRKAQEVPHSEKRF  
TRKSVVASQGFQAGRHYWEVDVGQNVGWWVGCRDDVDRGKNNVTLSNNNGYWVRLTTEHYFT  
FNPHFISLPPSTPPTRGVFLDYEGGTISFFNTNDQSLIYTLLTCQFEGLLRPYIQHAMYDEEKG  
TPIFICPVSWG

**Signal peptide:**

amino acids 1-17

**Transmembrane domains:**

amino acids 131-150, 235-259

## **FIGURE 105**

CCTTCACAGGACTCTCATTGCTGGTTGGCAATGATGTATCGGCCAGATGTGGTAGGGCTAGGAAAAGAG  
TTTGTGGGAACCCGGTTATCGGCTCGTCATCTTCATATCCCTGATTGTCCTGGCAGTGTGCATTGGA  
CTCACTGTTCATTATGTGAGATATAATCAAAGAAGACCTACAATTACTATAGCACATTGTCATTACAC  
TGACAAACTATATGCTGAGTTGGCAGAGAGGGCTCTAACAAATTACAGAAATGAGCCAGAGACTTGAAT  
CAATGGTGAAGGAAATGCATTAAACATCCATTAAAGGAAGAATTGTCAGTCTCAGGTTATCAAGGTT  
AGTCACAGAAGCAGTGGAGTGTGGCTCATATGCTGTTGATTGAGATTCACTCTACTGAGGATCCTGA  
AACTGTAGATAAAATTGTTCAACTTGTACATGAAAGCTGCAAGATGCTGTAGGACCCCTAAAGTAG  
ATCCTCACTCAGTAAATTAAAAAAATCAACAAGACAGAACAGACAGCTATCTAAACCATGCTGCGGA  
ACACGAAGAAGTAAACTCTAGGTAGAGTCTCAGGATCGTGGTGGACAGAAGTAGAGAAGAGGGTGAATG  
GCCCTGGCAGGCTAGCCTGCAGTGGGATGGAGTCATCGCTGTGGAGCAACCTTAATTAGCCACATGGC  
TTGTGAGTGTGCTCACTGTTTACAACATATAAGAACCCCTGCCAGATGGACTGCTTCCGGAGTAACA  
ATAAAACCTTCGAAATGAAACGGGTCTCCGGAGAATAATTGTCATGAAAATACAAACACCCATCACA  
TGACTATGATATTCTCTTGAGAGCTTCTAGCCCTGTTCCACACAAATGCAGTACATAGAGTTGTC  
TCCCTGATGCATCCTATGAGTTCAACCAGGTGATGTGATGTTGTGACAGGATTGGACACTGAAAAT  
GATGGTACAGTCAAAATCATCTCGACAAGCACAGGTGACTCTCATAGACGCTACAACCTGCAATGAACC  
TCAAGCTTACAATGACGCCATAACTCCTAGAATGTTATGCTGGCTCCTAGAAGGAAAACAGATGCAT  
GCCAGGGTGAICTGGAGGACACTGGTAGTCAGATGCTAGAGATATCTGGTACCTGCTGGAATAGTG  
AGCTGGGAGATGAATGTCGAAACCCAAACAAGCCTGGTTTACTAGAGTTACGCCCTGCGGGACTG  
GATTACTTCAAAAACGGTATCTAAGAGACAAAGCCTCATGGAACAGATAACATTTTGGTGTGACTGATCTCA  
ATAAAACTGTTGCTTGTGATGCTGTTCTAGAAGGTTGAGATACAGAATTGGAGAAGACTTGCAAAACAGCTAGATTGACTGATCTCA  
GATCAACTCTGTCATCTGTGAGCAATAGTTGAAACTTATGTCATAGAGAAATAGATAACATATTAC  
ATTACAGCCTGTATTCTAGAAGGTTGTCAGAATTGACTGACATAATTGTAAT  
GCATATATACAATTGAAAGCACTCCTTCTTCAGTCTCAGCTCCTCTCATTCTAGCAAATATCCATT  
TCAAGGGTGCAGAACAAAGGAGTGAAGAAAATATAAGAAGAAAAAAACCCCTACATTGTTATGGCACAGAA  
AAGTATAGGTGTTCTTAGTGGAAATTAGAAATGATCATATTCTAGGAAAGTGAAGAAGTCCAGAAAGCAG  
GCAGAACATCAACTCATCTAGAAGTATGGAAACTAAGTTAGGAAGTCCAGAAAGAAGCAG  
ATATATCCTATTTCATTTCAACAAACTACTATGATAATGTGAAGAAGATTGTTGACCT  
ATAATAATTATACAAACCTCATGCAATGTAATTGTTCTAAGCAAATTAAAGCAAATTATTTAACATTG  
TTACTGAGGATGTCAACATATAACAATAAAATATAACACCA

## **FIGURE 106**

MMYRPDVVRARKRVCWEPWVIGLVI FISLIVLAVCIGLT VHYVRYNQKKTYNYYSTLSFTTDKLY  
AEFGREASNNFTEMSQRLESMVKNAYKSPLEE FVKSQVIKFSQQKHGVLAHMLLICRFHSTED  
PETVDKIVQLVLHEKLQDAVGPPKVDPHSVKIKKINKTETDSYLNHCCGTRRSKTLGOSLRIVGG  
TEVEEGEWPWQASLQWDGSHRCGATLINATWLVSAAHCFTTYKNPARWTASFGVTIKPSKMKRGL  
RRIIVHEKYKHPHDYDISLAE LSSPV PYTNAVRVCLPDASYE FQPGDVMFVTGFGALKNDGYS  
QNHLRQAQVTLIDATT CNEPQAYNDAITPRMLCAGSLEGKTDACQGDGGPLVSSDARDIWYLAG  
IVSWGDEC A KPNKPGVYTRVTALRDWITSKTGI

**Transmembrane domain:**

amino acids 21-40 (type II)

## **FIGURE 107**

AGAGAAAGAAGCGCTCCAGCTGAAGCCAATGCAGCCCTCCGGCTCTCCCGAAGAAGTTCCCTG  
CCCCGATGAGCCCCCGCCGTGGCTCCCGACTATCCCCAGGCCGGCTGGGGCACCGGGCCCAGC  
GCCGACGATCGCTGCCGTTGCCCTGGGAGTAGGATGTGGTGAAGGATGGGCTTCTCCCT  
ACGGGGCTCACAA**TGGCCAGAGAAGATTCCGTGAAGTGTCTGCCTGCCTGCTCACGCCCTCAA**  
TCTGCTTTGGTTAATGTCATCAGTGTGGCAGTTCTGCTGGATGAGGGACTACCTAA  
ATAATGTTCTCACTTAACTGCAGAACAGAGGGTAGAGGAAGCAGTCATTGACTTACTTCCT  
GTGGTTCATCCGGTCATGATTGCTGTTGCTGTTCTATCATTGTTGGGATGTTAGGATATTG  
TGGAACGGTGAAAGAAATCTGTTGCTTCTGCATGGTACTTTGGAGTTGCTGTCAATTCT  
GTGTAGAACTGGCTGTGGCCTTGGACATATGAACAGGAACCTATGGTTCCAGTACAATGGCA  
GATATGGTCACTTGAAGGCCAGGATGACAAATTATGGATTACCTAGATATCGGTGGCTTACTCA  
TGCTTGAATTTCAGAGAGTTAAGTGTGGAGTAGTATATTCACTGACTGGTGG  
AAATGACAGAGATGGACTGGCCCCAGATTCCTGCTGTTAGAGAATTCCAGGATGTTCCAAA  
CAGGCCACCAGGAAGATCTCAGTGCACCTTATCAAGAGGGTTGTGGGAAGAAAATGTTCCCT  
TTTGAGAGGAACCAAACTGCAGGTGCTGAGGTTCTGGGAATCTCCATTGGGTGACACAAA  
TCCTGGCCATGATTCTCACCATTACTCTGCTCTGGGCTCTGTATTATGATAGAACGGAGCCTGGG  
ACAGACCAAATGATGTCCTGAAGAATGACAACCTCTCAGCACCTGTCTGCCCCAGTAGAACT  
GTTGAAACCAAGCTGTCAAGAATCTTGAACACACATCCATGGCAAACAGCTTAATACACACT  
TTGAGATGGAGGAGTT**AAAAAGAAATGT**CAAGAACAGAAAACCACAAACTTGTTTTATTGGACT  
TGTGAATTGGAGTACATACATGTGTTAGAAATATGTAGAAATAAAATGTTGCCATAAAA  
TAACACCTAAAGCATATACTATCTATGCTTAAATGAGGATGGAAAGTTCTGATGCTATAAGTC  
ACCACCTGGACAATAATGATGCCCTAAATGCTGAAGACAGATGTCATACCCACTGTGTAGCC  
TGTGTATGACTTTACTGACACAGTTGTTGAGGAGCATGGTTGATTAGCATTTCGGCA  
TCCATGCAAACGAGTCACATATGGTGGACTGGAGCCATAGTAAAGGTGATTACTCTACCAA  
CTAGTATATAAAAGTACTAATTAAATGCTAACATAGGAAGTTAGAAAATCTAAACTTTTATTAA  
CTCAGCGATCTATTCTCTGATGCTAAATAATTATGCTAACATAGGAAGTTAGAAAATCTCA  
ACCTAAATGTGATTGGTGTGGTTACTAAATAATTATGCTAACATAGGAAGTTAGAAAATCTCA  
TGTCTTAAGCTGATCAGGGATTGGTATATAAGTGTAAATCTGTTAAATCTGATAATTCA  
TTCACTGATAATTGTAAGAATAACCATTATGAAAGAAAATTGTCCTGTATAGCATCATT  
ATTGGTATTTAAATACTTAACCACTAATTGAAATTACCACTGTGATACTAGGAATCATTATTC  
TGTGTTAAATACTTAACCACTAATTGAAATTACCACTGTGATACTAGGAATCATTATTC  
AGAATGTTAGCTGGCTTGTGAAAGTTAGAATAAGAAAATTGCACTAAACTTGTGATT  
AAGGACTTGTATGCTGTTCTCCAAATGAAGACTTTTGACACTAAACACTTTTAAAAAA  
GCTTATCTTGCCTCTCCAAACAGAACAGAAATGCTCCAGTCAATATAAAATTCTACAGAAAA  
TAGTGTCTTTCTCCAGAAAATGCTGTGAGAATCATTAAACATGTGACAATTAGAGATT  
CTTGTGTTATTCACTGATTAATATACTGTGGCAAATTACACAGATTATTAAATTGGTTACAA  
GAGTATAGTATATTATTGAAATGGAAAAGTCATTTACTGTATTGTGATTGTTAT  
TTCTCAGAATATGAAAGAAAATTAAATGTGCAATAAAATTCTAGAGAGTAA

## **FIGURE 108**

MAREDSVKCLRCLLYALNLLFWLMSISVLAWSAWMRDYLNNVLTLTAETRVEEAVILTYFPVVHP  
VMIAVCCFLIIVGMLGYCGTVKRNLLLLAWYFGSLLVIFCVELACGVWTYEQELMVPVQWSDMVT  
LKARMTNYGLPRYRWLTHAWNFFQREFKCCGVVYFTDWLEMTEMDWPPDSCCVREFPGCSKQAHQ  
EDLSDLYQEGCGKKMYSFLRGTKQLQVLRFGLSIGVTQILAMILTITLLWALYYDRREPGTDQM  
MSLKNDNSQHLSCPSVELLKPSLSRIFEHTSMANSFNTHFEMEEL

**Signal peptide:**

amino acids 1-33

**Transmembrane domains:**

amino acids 12-35, 57-86, 94-114, 226-248

## FIGURE 109

CCAAGGCCAGAGCTGGACACCTTATCCCCTCATCCTCATCCTCTGATAAAGCCCCCTACCACTGCT  
GATAAAGTCTTCTCGTAGAGGCCTAGAGGCCTTAAAAAAAGTCTGAAAGAGAAGGGGACAAAGGAACA  
CCAGTATAAGAGGATTTCCAGTGTTCCTGGCAGTTGGTCCAGAAGGATGCCTCCATTCTGCTTCTCACCTG  
CCTCTTCATCACAGGCACCTCGTGTACCCGTGCCCTAGATCCTGTTCTGCTTACATCAGCCTGAATGAGC  
CCTGGAGGAACACTGACCACCACTGGATGAGTCTCAAGGTCTCTCTATGTGACAACCATGTGAATGGGAG  
TGGTACCACTTCACGGGCATGGCGGAGATGCCATGCCTACCTCTGCATACCAAGAAAACCACTGTGGAACCCA  
CGCACCTGCTGGCTCAATGGCAGCCACCCCTAGAAGGCAGGGATTGTGCAACGCCAGGCTGTGCCAGCT  
TCAATGGAACTGCTGTCTGGAACACCACGGTGGAAAGTCAAGGCTTGCCTGGAGGCTACTATGTGTATCGT  
CTGACCAAGCCCAGCGCTGCTTCCACGTCTACTGTGGTCAATTGACATCTGCGACGAGGACTGCCATGG  
CAGCTGCTCAGATAACCAGCGAGTGCACATGCGCTCCAGGAACACTGTGCTAGGCCCTGACAGGCAGACATGCTTG  
ATGAAAATGAATGTGAGCAAACACGGTGGCTGAGTGAAGACTCTGTGAAACCTCAAAACTCCTACCGCTGT  
GAGTGTGGGTTGGCGTGTGCTAAGAAGTGTGCAAGACACTTGTGAAGACGTTGAAGGATGCCACAATAACAA  
TGGTGGCTGCAGCCACTCTGGCTTGGATCTGAGAAAGCTACCGTGTGAATGTCCCCGGGCTGGTGT  
CTGAGGATAACCACACTTGCCTGGAGTCCCTGTGTTGCAATCAAATGCCATTGAAGTGAACATCCCCAGGGAG  
CTGGTTGGTGGCCTGGAGCTTCTGACCAACACCTCCGTGCCAGGAGTGTCCAACGGCACCCATGTCAACAT  
CCTCTCTCTCAAGACATGTGGTACAGTGGTCACTGTGGTGAATGACAAGATTGTGGCAGCAACCTCGTGA  
CAGGTCTACCCAAGCAGACCCGGGGAGCAGCGGGACTTCATCATCCGAACCAAGCAAGCTGCTGATCCCCGT  
ACCTGCGAGTTCCACGCCGTACACCATTCTGAAGGATACTGGTCAAGGACAATGAGTTGAAGACCTTACCC  
CATGAGCCGAAATCATGGATCTTCCATTCACTCTGGAGATCTCAAGGACAATGAGTTGAAGACCTTACCC  
GGGAAGCTCTGCCACCCCTCAAGCTCGTACTCCCTACTTGGCATTGAGCCCGTGGTGCACGTGAGCGGC  
TTGGAAAGCTTGGTGGAGAGCTGCTTGCACCCCACTCCAGGATCTGAGGAGTGTGACTGCCGGTTCTGT  
CCGGGATGGCTGTGTTCAAGATGACTCGGTAAGCAGTACACATCCGGGATCACCTAGCAAAGCACTCCAGG  
TCCCTGCTTCAAGTTGTGGCAAAGACCAAGGAAAGTGTGACTGCCGGTTCTGTGACTGCCGGTTCTGT  
TTGGACGAGCGTCCCGTGTGCCACCCGGAGTCCGCTGAGGAGTGTGACTGCCGGTTCTGTGACTGCC  
CGGTCTACAGGCCAGCGCTAACAGCGGCCGATCCGCATCGACTGGAGGACTAGTTCGTAGCCATACCTC  
GAGTCCCTGCATTGGACGGCTCTGCTCTGGAGCTCTCCCCCACTGGCCCTCAAGAACATCTGCCAACAGC  
TGGGTTCAAGCTTCAACTGTGAGTTCAAGACTCCAGCACCAACTCACTGATTCTGGTCCATTCACTGGCA  
CAGGTCAAGCACTGCTGAACAATGTGGCTGGGTGGGTTCATCTTCTAGGGTGAAAACAAACTAACTGTCCA  
CCCAGAAAGACACTCACCCATTCCCTCATTCTTCCCTACACTTAAACCTCGTGTATGGTGCAATCAGAC  
CACAAAATCAGAAGCTGGGTATAATATTCAAGTTACAACCCAGAAAAATTAAACAGTTACTGAAATTATGA  
CTTAAATACCAATGACTCCTTAAATATGTAATTAGTTACCTGAAATTCAATTCAAATGCAGACTAA  
TTATAGGAATTGGAAAGTGTATCAATAAAACAGTATATAATT

## **FIGURE 110**

MPPFLLTCLFITGTSVSPVALDPCSAYISLNEPWRNTDHQIDESQGPPLCDNHVNGEWYHFTGMAGDAMP  
TFCIPENHCGTHAPVWLNGSHPLEGDGIVQRQACASFNGNCCLWNTTVEVKACPGYYVYRLTKPSVCFHV  
YCGHFYDICDEDCHGCSDTSECTCAPGTVLGPDRQTCFDENECEQNNGGCSEICVNLKNSYRCECGVGRV  
LRSDBGKTCEDVEGCHNNNGGSHSCLGSEKGYQCECPRLVLSEDNHTCQVPVLCKSNAIEVNIPRELVGG  
LELFFLTNTSCRGVSNGTHVNILFSLKTCGTVVNDKIVASNLVTGLPKQTPGSSGDFIIRTSKLLIPVT  
CEFPRPLYTISEGYVPNLRNSPLEIMSRNHGIFPFTLEIFKDNEFEYPYREALPTLKLRLDSLYFGIEPVVHV  
SGLESLVESCFTPTSKIDEVLKYYLIRDGCVSDDSVKQYTSRDHLAKHFQVPVFKFVGKDHKEVFLHCRV  
LVCGVLDERSRCAQGCHRRMRRGAGGEDSAGLQGQTLTGGPIRIDWED

**Important features of the protein:**

**Signal peptide:**

amino acids 1-16

**N-glycosylation sites.**

amino acids 89-93, 116-120, 259-263, 291-295, 299-303

**Tyrosine kinase phosphorylation sites.**

amino acids 411-418, 443-451

**N-myristoylation sites.**

amino acids 226-232, 233-239, 240-246, 252-258, 296-302, 300-306,  
522-528, 531-537

**Aspartic acid and asparagine hydroxylation site.**

amino acids 197-209

**ZP domain proteins.**

amino acids 431-457

**Calcium-binding EGF-like proteins.**

amino acids 191-212, 232-253

## **FIGURE 111**

GAGAGAGGCAGCAGCTGCTAGCGGACAAGGATGCTGGGCGTAGGGACCAAGGCCTGCCCTGCACTCGG  
GCCTCCCTCAGCCAGTGTGACCAGGGACTCTGACCTGCTGGCAGCCAGGACCTGTGTGGGAGGCCT  
CCTGCTGCCCTGGGGTACAATCTCAGCTCCAGGCTACAGGGAGACCGGGAGGATCACAGAGCCAGC**ATGT**  
TACAGGATCCTGACAGTGATCAACCTCTGAACAGCCTCGATGTCAAACCCCTGCGCAAACCCCGTATCCCC  
ATGGAGACCTTCAGAAAGTGGGATCCCATCATCATAGCACTACTGAGCCTGGCAGTATCATCATTTGT  
GGTTGTCCATCAAGGTGATTCTGGATAAAACTACTTCCTCTGCGGGCAGCCTCTCCACTTCATCCGA  
GGAAGCAGCTGTGTGACGGAGAGCTGGACTGTCCTGGGGAGGACGAGGAGCACTGTGTCAAGAGCTTC  
CCCGAAGGGCCTGCAGTGCAGTCGCCTCTCAAGGACCGATCCACACTGCAGGTGTGGACTGCCAC  
AGGGAACCTGGTCTCGCCTGTTGACAACACTTCACAGAACGCTCGCTGAGACAGCCTGTAGGCAGATGG  
GCTACAGCAGAGCTGTGGAGATTGGCCAGACAGGATCTGGATGTTGTAATCACAGAAAACAGCCAG  
GAGCTTCGATCGGAAACTCAAGTGGCCCTGTCCTCAGGCTCCCTGGCTCCCTGCACTGTCTGCC  
TGGGAAGAGCCTGAAGACCCCCCGTGTGGTGGGGAGGAGGACATCCTGGACCCCCACTGGCTCAGGG  
TCAGCATCCAGTACGACAAACAGCACGTCTGGAGGGAGCATTGGACCCCCACTGGCTCAGGG  
GCCCACTGCTCAGGAAACATACCGATGTGTTCAACTGGAAGGTGCGGGCAGGCTCAGACAAACTGGCAG  
CTTCCCATCCCTGGCTGTGGCAAGATCATCATATTGAATTCAACCCATGTACCCAAAGACAATGACA  
TCGCCCTCATGAAGCTGCAGTCCCACACTCACTTCTCAGGCACAGTCAGGCCATCTGTCTGCC  
GATGAGGAGCTCACTCCAGCCACCCACTCTGGATATTGGATGGGCTTACGAAGCAGAATGGAGGGAA  
GATGTCGACATACTGCTGCAGGCTCAGTCCAGGTATTGACAGCACACGGTGAATGCAAGCAGATGCGT  
ACCAGGGGAAGTCACCGAGAAGATGATGTGTGCAGGCATCCCGGAAGGGGTGTGGACACCTGCCAGGG  
GACAGTGGTGGGCCCTGATGTAACCAATCTGACCAACTGGCATGTGGTGGCATCGTTAGCTGGGCTATGG  
CTGGGGGGGCCGAGCACCCCAGGAGTATACACCAAGGTCTAGCCTATCTCAACTGGATCTACAATGTCT  
GGAAAGGCTGAGCTG**TAAT**GCTGCTGCCCTTGCAGTGTGGAGGCCCTTCCCTGCCCTGCCACCT  
GGGATCCCCAAAGTCAGACACAGAGCAAGAGTCCCTGGTACACCCCTCTGCCACAGCCTCAGCAT  
TTCTGGAGCAGCAAAGGGCCTCAATTCTGTAAGAGACCCCTCGCAGCCAGGGCGCCAGAGGAAGTCA  
GCAGCCCTAGCTGGCCACACTTGGTGTCCAGCATCCCAGGGAGAGACACAGCCACTGAACAAGGTCT  
CAGGGGTATTGCTAAGCCAAGAAGGAACCTTCCCACACTACTGAATGGAAGCAGGCTGTCTGTAAAAGCC  
CAGATCACTGTGGCTGGAGAGGAGAAGGAAAGGGTCTGCCAGCCCTGTCCGTCTCACCCATCCCCAA  
GCCTACTAGAGCAAGAACCAGTTGTAATATAAAATGCACTGCCCTACTGTTGGTATGACTACCGTACCT  
ACTGTTGTCATTGTTATTACAGCTATGCCACTATTATAAGAGCTGTAAACATCTGGCAAAAAAAA  
AAAA

## **FIGURE 112**

MLQDPDSDQPLNSLDVKPLRKPRIPMETFRKVGIP III I ALLSLASIIIVVLIKVILDKYYFLCG  
QPLHFIPRKQLCDGELDCPLGEDEEHCVKS FPEGPAVAVRLSKDRSTLQVLDSATGNWFSACFDN  
FTEALAAETACRQMGSRAVEIGPDQDLDVVEITENSQELMRMRNSSGPGCLSGSLVSLHCLACGKSL  
KTPR VVGEEASVDSWPWQVS IQYDKQHVCGGSILDPHWLTAAHCFRKHTDVFNWKRAGSDKL  
GSFPSLAVAKIIIIEFNPMYPKDNDIALMKLQFPLTFSGTVRPICLPPFDEELTPATPLWIIWG  
FTKQNGGKMSDILLQASVQVIDSTRCNADDAYQGEVTEKMMCAGIPEGGVDTQGDGGPLMYQS  
DQWHVVGIVSWGYGCGGPSTPGVYTKVSAYLNWIYNVWKAEL

**Transmembrane domain:**

amino acids 32-53 (typeII)

### **FIGURE 113**

GGCTGGACTGGAACCTCTGGTCCAAGTGATCCACCCGCCTCAGCCTCCAAAGGTGCTGTGATTA  
TAGGTGTAAGCCACCGTGTCTGCCCTGAACAACCTTTCACTGCTGCTACCTACATTAAAATC  
TGAACTGCTAGGATTCTGACTATGCTGTGGCTAGTGCCTACTCCTACCTACATTAAAATC  
TGTGTTTGTCTCTGTAACTAGCCTTACCTCCTAACACAGAGGATCTGTCAGTGTGGCTCT  
GGCCCAAACCTGACCTCACTCTGGAACGAGAACAGAGGTTCTACCCACACCGTCCCCTGAAG  
CCGGGGACAGCCTCACCTGCTGGCCTCTCGCTGGAGCAGTGCCTCACCAACTGTCACGTCT  
GGAGGCAGTGACTCGGGCAGTGCAAGGTAGCTGAGCCTCTGGTAGCTGCGGCTTCAGGTGGC  
CTTGCCCTGGCGTAGAAGGGATTGACAAGCCGAAGATTCACTAGGCATGGCTCCACTGCC  
AGGCATCAGCCTGCTGAGTCATCACTGCCCTGGGCCAGGACGGGCGTGGACACCTGCTCA  
GAAGCAGTGGGTGAGACATCACGCTGCCGCCATCTAACCTTCACTGTCCTGCACATCACCTG  
ATCCATGGGCTAACCTGAACCTGTCCCAAGGAACCCAGAGCTTGAGTGGCTCAGACC  
CAGAAGGGGCTGCTTAGACCACCTGGTTATGTGACAGGACTTGCATTCTCCTGGAACATGAGG  
GAACGCCGGAGGAAAGCAAAGTGGCAGGGAAAGGAACCTGTGCCAAATTATGGGTCAAGAAAGATG  
GAGGTGTTGGTTATCACAAGGCATCGAGTCTCCTGCATTCACTGAGCTGAGTGGCTCAGACC  
CCGATGGCGCATGACACACTCGGGACTCACCTCTGGGCCATCAGACAGCGTTCCGCCCGAT  
CCACGTACCGACTGCTGAAGGGCAACTGCAGGCCATGCTCATCAGCCAGGCGAGCAGCCAAA  
TCTGCGATCACCAGCCAGGGCAGCCGTGGAGGAGCAAGCAAAGTGACCTCTCCCTCC  
CTCCTCCCTCTGAGAGGCCCTCTATGTCCTACTAAAGCCACCAGCAAGACATAGCTGACAGG  
GGCTAACGGCTCAGTGTGGCCAGGAGGTCAAGCAAGGCTGAGAGCTGATCAGAAGGCCCTGCT  
GTGCGAACACGGAAATGCCCTCAGTAAGCACAGGCTGCAAATCCCAGGCAAAGGACTGTGTGG  
CTCAATTAAATCATGTTCTAGTAATTGGAGCTGTCCCAAGACCAAAGGAGCTAGAGCTTGGTT  
CAAATGATCTCAAGGGCCTTATACCCAGGAGACTTGAATTGAAACCCCAAATCCA  
AACCTAAGAACCAAGGTGCATTAAGAACATCAGTTATTGCCGGGTGTGGCTGTAATGCCAACATGG  
TTTGGGAGGCCAGGGTAGATCACCTGAGGTCAAGGAGCTCAAGACCCAGGCCAACATGG  
TGAAACCCCTGTCTACTAAAAACAAAAAACTAGCCAGGCAAGGTGTGGCTGTATC  
CCAGCTACTCGGGAGGCTGAGACAGGAGAATTACTGAAACCTGGAGGTGAAGGAGGCTGAGACA  
GGAGAACATCACTCAGCCTGAGCAACACAGCGAGACTCTGTCAGAAAAAATAAAAAAAGAATTA  
TGGTTATTTGTAA

## **FIGURE 114**

MLWWLVLLLPTLKSVFCSLVTSLYLPNTEDSLWLPKPDLHSGTRTEVSTHTVPSKPGTASPC  
WPLAGAVPSPTVSRLEALTRAVQVAEPLGSCGFQGGPCPGRRRD

**Signal peptide:**

amino acids 1-15

## **FIGURE 115**

CAGCAGTGGTCTCTAGCCTCTCAAAGCAAGGAAAGAGTACTGTGTGCTGAGAGACCATGGCAA  
AGAATCCTCCAGAGAATTGTGAAGACTGTACATTCTAAATGCAGAAGCTTTAAATCCAAGAAA  
ATATGTAATCACTTAAGATTGTGGACTGGTGTGTTGATCCTGGCCCTAACCTCTAAATTGTCT  
GTTTGGGGAGCAAGCACTTCTGGCCGGAGGTACCCAAAAAGCCTATGACATGGAGCACACTT  
TCTACAGCAATGGAGAGAAGAAGAAGATTACATGGAAATTGATCCTGTGACCAGAACTGAAATA  
TTCAGAAGCGAAATGGCACTGATGAAACATTGAAAGTGCACGACTTTAAAACGGATAACTGG  
CATCTACTCGTGGGTCTCAAAATGTTTATCAAACACTCAGATTAAGTGATTCTGAATTT  
CTGAACCAGAAGAGGAAATAGATGAGAATGAAGAAATTACCAACTTCTTGAAACAGTCAGTG  
ATTGGGTCCCAGCAGAAAGCCTATTGAAACCGAGATTCTCTTAAAATTCCAAAATTCTGGA  
GATTTGTGATAACGTGACCATGTATTGGATCAATCCACTCTAAATATCAGTTCTGAGTTACAAG  
ACTTTGAGGAGGGAGGAGAAGATCTTCACCTTCTGCCAACGAAAAAAAAGGGATTGAACAAAAT  
GAACAGTGGTGGTCCCTCAAGTGAAGTAGAGAAGACCCGTACGCCAGACAAGCAAGTGAGGA  
AGAACTCCAATAATGACTATACTGAAATGGAATAGAATTGATCCCATGCTGGATGAGAGAG  
GTTATTGTTGATTACTGCCGTGAGGCAACCGCTATTGCCGCCGTCTGTGAACCTTACTA  
GGCTACTACCCATATCCACTGCTACCAAGGAGGACGAGTCATCTGCGTGTATCATGCCCTG  
TAACTGGTGGTGGCGCCGCATGCTGGGGAGGGTCTAATAGGAGGTTGAGCTCAAATGCTTAAAC  
TGCTGGCAACATATAATAATGATGCTATTCAATGAATTCTGCCTATGAGGCATCTGGCCCT  
GGTAGCCAGCTCCAGAATTACTGTAGGTAATTCTCTCTTCATGTTCTAAACTTCTACA  
TTATCACCAAAAAAAAAAAAAAA

## **FIGURE 116**

MAKNPPENCEDCHILNAEAFSKKICKSLKICGLVFGILALTILFWGSKHFPEVPKKAYDME  
HTFYNSNGEKKKIYMEIDPVTRTEIFRSGNGTDETLEVHDFKNGYTGIYFVGLQKCFIKTQIKVIP  
EFSEPEEEIDENEITTTFFEQSVIWVPAEKPIENRDFLKN SKILEICDNVTMYWINPTLISVSE  
LQDFEEEGEDLHFPANEKKGIEQNEQWVVPQVKVEKTRHARQASEEEELPINDYTENGIEFDPMED  
ERGYCCIYCRRGNRYCRRVCEPLLGYYPYCYQGGRVICRVIMPCNWWVARMLGRV

**Important features of the protein:**

**Signal peptide:**

amino acids 1-40

**Transmembrane domain:**

amino acids 25-47 (type II)

**N-glycosylation sites.**

amino acids 94-97, 180-183

**Glycosaminoglycan attachment sites.**

amino acids 92-95, 70-73, 85-88, 133-136, 148-151, 192-195, 239-  
242

**N-myristylation sites.**

amino acids 33-38, 95-100, 116-121, 215-220, 272-277

**Microbodies C-terminal targeting signal.**

amino acids 315-317

**Cytochrome c family heme-binding site signature.**

amino acids 9-14

## **FIGURE 117**

GAGCTCCCTCAGGAGCGCGTTAGCTTCACACCTTCGGCAGCAGGAGGGCGGCAGCTCTCGCAGGCGGCA  
GGCGGGCGGCCAGGATCATGTCCACCACCATGCCAAGTGGTGGCGTCCCTGCATCCTGGGCT  
GGCGGCTGCATCGCGGCCACCGGGATGGACATGTGGAGCACCAGGACCTGTACGACAACCCCGTCACCT  
CCGTGTTCCAGTACGAAGGGCTCTGGAGGAGCTCGTGAGGCAGAGTTCAGGCTTCACCGAATGCAGGCC  
TATTTACCATCCTGGACTTCAGCCATGTCAGGCAGTGCGAGCCCTGATGATCTAGGCATCGCCT  
GGGTGCCATTGGCCTCTGGTATCCATCTTGCCTGAAATGCATCCGCATTGGCAGCATGGAGGACTCTG  
CCAAAGCCAACATGACACTGACCTCCGGATCATGTTCAATTGTCAGGTCTTGTGCAATTGCTGGAGTG  
TCTGTGTTGCCAACATGCTGGTACTAACTCTGGATGTCACAGCTAACATGTACACCGGATGGTGG  
GATGGTGCAGACTGTTCAAGACCAGGTACACATTGGTGCCTGTTGCGGCTGGCTGGCTGGAGGCC  
TCACACTAACATTGGGGGTGTGATGATGTGCATGCCCTGCCGGGCTGGCACCAGAAGAAACCAACTACAAA  
GCCGTTCTTATCATGCCCTCAGGCCACAGTGGTGCCTACAAGCCTGGAGGCTCAAGGCCAGCACTGGCTT  
TGGGTCCAACACCAAAAAACAAGAAGATATACTGATGGAGGTGCCGCACAGAGGACGAGGTACAATCTATC  
CTTCCAAGCAGACTATGTGTAATGCTCTAACGACCTCTCAGCACGGCGGAAGAAAACCTCCGGAGAGCTA  
CCCCAAAACAAGGAGATCCCATCTAGATTCTCTGCTTTGACTCACAGCTGAAAGTTAGAAAAGCCT  
CGATTCATCTTGGAGAGGCCAATGGTCTTAGCCTCAGTCTGCTCTAAATATTCCACCATAAAACA  
GCTGAGTTATTATGAATTAGAGGCTATAGCTCACATTTCACATCCTCTAAATATTCTTTAAATATAACT  
TTCTACTCTGATGAGAGAATGTGGTTTAATCTCTCTCACATTGATGATTTAGACAGACTCCCCCTC  
TTCCTCTAGTCAATAAACCCATTGATGATCTATTCCAGCTATCCCCAGAAAACCTTTGAAAGGAAA  
GAGTAGACCCAAAGATGTTATTTCTGCTGTTGAATTGTCTCCCCACCCCAACTGGCTAGTAATAA  
ACACTTACTGAAGAAGAAGCAATAAGAGAAAGATATTGTAATCTCTCCAGGCCATGATCTGGTTCT  
ACACTGTGATCTAAAGTTACCAACCAAAAGTCATTTCAGTTGAGGCAACCAACCTTCTACTGCTG  
TTGACATCTCTTATTACAGCAACACCATTCTAGGAGTTCTGAGCTCTCCACTGGAGTCCTTTCTG  
CGCGGGTCAGAAATTGCTCTAGATGAATGAGAAAATTATTTTTAATTAAAGTCCTAAATATAAGTTAA  
AATAAAATAATGTTAGTAAAATGATACACTATCTCTGAAATAGCCTACCCCTACATGTGGATAGAAG  
GAAATGAAAAAATAATTGCTTTGACATTGTCATATGGTACTTTGAAAGTCATGCTTAAGTACAAATTCC  
ATGAAAAGCTCACACCTGTAATCTGACTTTGGGAGGCTGAGGAGGAAGGACTGAGCCAGAAGT  
TCGAGACTAGCCTGGCAACATGGAGAAGCCCTGCTCTACAAATACAGAGAGAAAAATCAGCCAGTCA  
TGGTGGCATACACCTGTAATGCTCAGCTCCGGAGGCTGAGGTGGGAGGATCACTTGAGCCCAGGGAGGT  
TGGGGCTGCACTGAGCCATGATCACACCAACTGCACTCCAGCCAGGTGACATAGCGAGATCCTGTCTAAAAA  
AATAAAAATAATAATGAAACACAGCAAGTCCTAGGAAGTAGGTTAAAACATAATTCTTAA

## **FIGURE 118**

MSTTCQVVAFLLSILGLAGCIAATGMDMWSTQDLYDNPVTSVFQYEGLWRSCVRQSSGFTECRP  
YFTILGLPAMLQAVRALMIVGIVLGAIGLLVSIFALKCIRIGSMEDSAKANMTLTSGIMFIVSGL  
CAIAGVSVFANMLVTNFWMSTANMYTGMGGMVQTVQTRYTFGAALFVGWVAGGLTLIGGVMMCIA  
CRGLAPEETNYKAVSYHASGHSVAYKPGGFKASTGFGSNTKNKKIYDGGARTEDEVQSYP SKHDY  
V

**Signal peptide:**

amino acids 1-23

**Transmembrane domains:**

amino acids 81-100, 121-141, 173-194

## **FIGURE 119**

GGAAAAACTGTTCTCTGTGGCACAGAGAACCTGCTCAAAGCAGAAGTAGCAGTCCGGAGTCC  
AGCTGGCTAAAACATCCCAGAGGATAATGGCAACCCATGCCTTAGAAATCGCTGGCTTTCTTG  
GTGGTGTGGAATGGTGGGCACAGTGGCTGCACTGTCATGCCTCAGTGGAGAGTGTGCGGCCTTCATT  
GAAAACAACATCGTGGTTTGAAAACCTCTGGAGGGACTGTGGATGAATTGCGTGAGGCAGGCTAA  
CATCAGGATGCAGTGCAAAATCTATGATTCCCTGCTGGCTTTCTCCGGACCTACAGGCAGCAG  
GACTGATGTGCTGCTCCGTGATGTCCTTCTGGCTTCATGATGCCATCCTGGCATGAAATGC  
ACCAGGTGCACGGGGACAATGAGAAGGTGAAGGCTCACATTCTGCTGACGGCTGGAATCATCTCAT  
CATCACGGGCATGGTGGTGCTCATCCCTGAGCTGGGTTGCCAATGCCATCATCAGAGATTCTATA  
ACTCAATAGTGAATGTTGCCAAAAACGTGAGCTGGAGAAGCTCTACTTAGGATGGACCACGGCA  
CTGGTGCTGATTGTTGGAGGAGCTCTGTTCTGCTGCGTTTGTGCAACGAAAAGAGCAGTAGCTA  
CAGATACTCGATACCTTCCCACGCACAACCCAAAAAGTTACACACGGAAAAGACTCACCGAGCG  
TCTACTCCAGAAGTCAGTATGTGTAGTTGTATGTTTTAACTTAACTAAAGCCATGCAAATG  
ACAAAAATCTATATTACTTCTCAAAATGGACCCCAAAAGAAACCTTGATTACTGTTCTTAACGCT  
AACTTAATTACAGGAACGTGCACTCAGCTATTATGATTCTATAAGCTATTCTAGCAGAATGAGATA  
TTAAACCCAAATGCTTGTGATTGTTCTAGAAAGTATAGTAATTGTTCTAAGGTGGTCAAGCATCTA  
CTCTTTTATCTTACTTCAAAATGACATTGCTAAAGACTGCATTATTTACTACTGTAATTCTCC  
ACGACATAGCATTATGTACATAGATGAGTGTAAACATTATCTCACATAGAGACATGCTTATATGGT  
TTTATTAAAGAAATGCCAGTCCATTACACTGAATAAATAGAACTCAACTATTGTTTCAGGGAA  
ATCATGGATAGGGTGAAGAAGGTTACTATTAAATTGTTAAAAACAGCTAGGGATAATGCTTCCA  
TTTATAATGAAGATTAAATGAAGGCTTAACTCAGCATTGTAAGGAAATTGAATGGCTTCTGATAT  
GCTGTTTTAGCCTAGGAGTTAGAAATCCTAACTCTTATCCTCTCCAGAGGCTTTTT  
CTTGTGTTAAATTAAACATTAAACAGCAGATATTGTCAAGGGCTTGCATTCAAAGCT  
TTCCAGGGCTACTCAGAAGAAAGATAAAAGTGTGATCTAAGAAAAGTGTGTTAGGAAAGT  
AAAATTTTGTGTTGTATTGAAGAAGAATGATGCAATTGACAAGAAATCATATATGTATGGAT  
ATATTAAATAAGTATTGAGTACAGACTTGAGGTTCATCAATATAAAAGAGCAGAAAATA  
TGTCTGGTTTCAATTGCTTACCAAAAAACAAACAACAAAAAAAGTTGCTTGTGAGAAACTCACCT  
GCTCCTATGTGGGTACCTGAGTCAGTCAAAATTGTCATTGTTCTGTGAAAATAATTCTCTGT  
CCATTCTGTTAGTTACTAAAATGTAAATACTGTATTGTTCTGTTATTCAAATTGATGAA  
ACTGACAATCCAATTGAAAGTTGTCGACGTCTGTCTAGCTTAAATGAATGTGTTCTATTGCTT  
TATACATTATTAATAAAATTGTACATTCTAATT

## **FIGURE 120**

MATHALEIAGLFLGGVGMVGTAVTVMPQWRVSAFIENNIVVFENFWEGLWMNCVRQANIRMQCK  
IYDSLLALSPDLQAARGLMCAASVMSFLAFMAILGMKCTRCTGDNEKVKAHILLTAGIIFIITG  
MVVLIPSWVANAIIRDYNSIVNVAQKRELGEALYLGWTALVLIVGGALFCCVFCCNEKSSSY  
RYSIPSHRTTQKSYHTGKKSPSVYSRSQYV

**Signal peptide:**

amino acids 1-17

**Transmembrane domains:**

amino acids 82-101, 118-145, 164-188

## **FIGURE 121**

GGAGAGAGGCGCGCGGGTGAAAGGCGATTGATGCAGCCTCGGGCGGCCTCGGAGCGCGGGAG  
CCAGACGCTGACCACGTTCTCCTCGGTCTCCCGCTCCAGCTCCCGCTGCCGGCAGCC  
GGGAGCCATGCGACCCCAGGGCCCCGCCCTCCCGCAGCGGCTCCCGGCCCTCGCTGCC  
TGCTGCTGCAGCTGCCCGCGCGTCAAGCGCCTCTGAGATCCCCAAGGGGAAGCAAAAGGCCAG  
CTCCGGCAGAGGGAGGTGGTGGACCTGTATAATGGAATGTGCTTACAAGGGCCAGCAGGAGTGCC  
TGGTCGAGACGGGAGCCCTGGGGCCAATGTTATTCCGGTACACCTGGGATCCCAGGTGGATG  
GATTCAAAGGAGAAAAGGGGGAAATGTCGAGGGAAAGCTTGAGGGACTCTGGACACCCAAC  
AAGCAGTGTTCATGGAGTTCAATTGAATTATGGCATAGATCTGGAAAATTGCGGAGTGTACATT  
TACAAAGATGCGTTCAAATAGTGTCTAAGAGTTGTTCACTGGCTCACTTGGCTAAAATGCA  
GAAATGCATGCTGTCAAGCGTTGGTATTTCACATTCAATGGAGCTGAATGTTCAAGGACCTCTCCC  
ATTGAAGCTATAATTATTGGACCAAGGAAGGCCCTGAAATGAATTCAACAATTAAATTATCATCG  
CACTTCTCTGTGGAAGGACTTGTGAAGGAATTGGTGGATTAGTGGATGTTGCTATCTGGG  
TTGGCAGTGTTCAGATTACCCAAAAGGAGATGCTTCACTGGATGGAATTCACTGGCTTCGACATC  
ATTATTGAAGAACTACCAAAAAATGCTTAATTTCATTTGCTACCTTTTTTATTATGCC  
TTGGAATGGTTCACTTAAATGACATTAAATAAGTTATGTATACTGAATGAAAAGCAAAG  
CTAAATATGTTACAGACCAAAGTGTGATTCACTGTTAAATCTAGCATTATTCAATTG  
CTTCAATCAAAAGTGGTTCAATTTCAGTTGTTAGAATACTTCTCATAGTCACATT  
CTCTCAACCTATAATTGGAATATTGTTGGTCTTTGTTCTTAGTATAGCATTGTTA  
AAAAAAATATAAAAGCTACCAATCTTGTACAATTGTTAAATGTTAAGAATTTCATATCTGT  
TAAATAAAAATTATTCCAACA

## **FIGURE 122**

MRPQGPAASPQRLRGLLLLLQLPAPSSASEIPKGKQKAQLRQREVVDLYNGMCLQGPAGVPGR  
DGSPGANVIPGTPGIPGRDGFKEKGECLRESFEESWTPNYKQCSWSSLNYGIDLGKIAECTFTK  
MRSNSALRVLFGSLLRKCRNACCQRWYFTFNGAECSGPLPIEAIYLDQGSPEMNSTINIHRTS  
SVEGLCEGIGAGLVVDVIAIWVGTCSDYPKGDASTGWNSVSRIIIIEELPK

**Signal peptide:**

amino acids 1-30

**Transmembrane domain:**

amino acids 195-217

## **FIGURE 123**

GCTGAGCGTGTGCGCGTACGGGCTCTCTGCCTCTGGCTCCAACGCAGCTGTGGCTGAA  
CTGGGTGCTCATCAGGGAACTGCTGGCTATGAAATACAGATGTGGCAGCTCAGGTAGCCCCAA  
ATTGCCTGGAAGAACATCATCATGTTTCGATAAGAAGAAATTGTAGGATCCAGTTTTTTTA  
ACCGCCCCCTCCCCACCCCCCAAAAAACTGTAAGAGATGCAAAACGTAATATCATGAAGATCC  
TATTACCTAGGAAGATTGATTTGATGCTGCGAATGCGGTGTTGGATTATTGTTCTGGAG  
TGGTCTGGTGGCTGGCAAAGAACATAATGTTCCAAAATCGGTCCATCTCCAAGGGTCCAATT  
TCTTCCTGGGTGTCAGCGAGCCCTGACTCACTACAGTGACGCTGACAGGGCTGTCATGCAACTG  
GCCCTAAAGCCAAAGCAAAAGACCTAAGGACGACCTTGAACAATACAAAGGATGGGTTCAATG  
TAATTAGGCTACTGAGCGGATCAGCTGAGCACTGGTTAGGCCCCACTGTCTACTGACAATG  
CTTTCTCTGCCGAACGAGGATGCCCTAAGGGCTGTAGGTGTGAAGGCAAAATGGTATATTGTA  
ATCTCAGAACATTACAGGAGATACCCCTCAAGTATATCTGCTGGTGTAGGTTGTCCTCGCT  
ATAACAGCCTCAAAACTTAAGTATAATCAATTAAAGGGCTCAACCAGCTCACCTGGCTATAC  
CTTGACCATAACCATATCAGCAATATTGACGAAAATGCTTTAATGGAATACGCAAGACTCAAAGA  
GCTGATTCTAGTCCAATAGAATCTCTATTCTAACATACCTCAGACCTGTGACAATT  
TACGGAACCTGGATCTGCTATACTAGCTGCATTCTGGATCTGAACAGTTGGGGCTT  
CGGAAGCTGCTGAGTTACATTACGGCTAACCTGGAGCTGGATATAACGGATCCGAAGTTAGCCAGGAATG  
AGACTGCCAACCTGGAACTTGGACCTGGGATATAACGGATCCGAAGTTAGCCAGGAATG  
TCTTGCTGGCATGACTCAAGAACATTACCTGGAGCACAATCAATTCTCAAGCTCAC  
CTGGCCCTTTCCAAGGTTGGTCAGCCTTCAGAACCTTACTTGCAGTGGAAATAAATCAGTGT  
CATAGGACAGACCATGTCCTGGACCTGGAGCTCTAACAAAGGCTTGATTTATCAGGCAATGAGA  
TCGAAGCTTCAGTGGACCCAGTGTGTTCCAGTGTGTCCGAATCTGCAGCGCTCAACCTGGAT  
TCCAACAAGCTCACATTATTGGTCAAGAGATTGGATTCTGGATATCCCTCAATGACATCAG  
TCTTGCTGGAAATATGGGAATGCAAGCAGAAATATTGCTCCCTGTAACCTGGCTGAAAGTT  
TTAAAGGTCTAAGGGAGAATACAATTATCTGTCAGTCCAAAGAGCTGCAAGGAGTAAATGTG  
ATCGATGCACTGAGAAACTACAGCATCTGTCAGTCCAAAGAGCTACAGAGGTTGATCTGGCAG  
GGCTCTCCAAAGCCGACGTTAACGCCAACGCTCCAGGCCAGAGACCGATGCTGACGCCAGCACATCT  
TGCCCCCGACGGTGGGAGGCCACAGAGCCCCAGAGACCGATGCTGACGCCAGCACATCT  
TTCCATAAAATCATCGCGGGCAGCGTGGCCTTCTCGTCCGTGTCGTGTCATCTGCTGGTT  
CTACGTTGTCATGGAAAGCGGTACCCCTGCGAGCATGAAGCAGCTGCAAGCGCTCCCTCATGCAA  
GGCACAGGAAAAAGAACACCGAGACCGAGATGCTGCTGAATGGGACGGGACCCCTGCACCTA  
GATTATAAAACCCACCAACACGGAGACCGAGATGCTGCTGAATGGGACGGGACCCCTGCACCTA  
TAACAAATCGGCTCCAGGGAGTGTGAGGTATGAACTATTGATAAAAGAGCTTAAAG  
GGGAAATAAGTGGCTTTATTGAACCTGGTGAATCAAGGGAAACGCGATGCCCTCCCTCC  
TTCCCTCTCCCTCACTTGGCAAGATCCTCCCTGTCGTTTAGTGCATTCAATAACT  
GGTCATTTCCTCTCATACATAATCAACCCATTGAAATTAAATACCACAATCAATGTGAAGCT  
GAACCTCGGTTAATATAATACCTATTGTATAAGACCCTTACTGATTCCATTATGTCGCA  
GTTTAAGATAAAACTCTTCATAGGTAAAAAAAAAA

## **FIGURE 124**

MGFNVIRLLSGSAVALVIAPTVLLMLSSAERGCPKGCRCEGKMYCESQKLQEIPSSISAGCLG  
LSLRYNSQLQKLKYNQFKGLNQLTWLYLDHNHISNIDENAFNGIRRLKELILSSNRISYFLNNNTFR  
PVTNLRNLDLSYNQLHSLGSEQFRGLRKLLSLHLSNSLRTIPVRIFQDCRNLELLDLGYNRIRS  
LARNVFAGMIRLKELHLEHNQFSKLNLALFPRLVSLQNLQWNKISVIGQTMSTWSSLQRSDL  
SGNEIEAFSGPSVFQCVPNLQRLNLDNSNKLFIGQEILDWSWISLNDISLAGNIWECSRNICS LVN  
WLKSFKGLRENTIICASPKELQGVNVIDAVKNYSICGKSTTERFDLARALPKPTFKPKLPRPKHE  
SKPPLPPTVGATEPGPETDADAEHISFHKIAAGSVALFLSVL VILLVIYVSWKRYPASMKQLOQR  
SLMRRHRKKRQSLKQMTPSTQEFYVDYKPTNTETSEMLLNGTGPCTYNKSGSRECEV

**Important features of the protein:**

**Signal peptide:**

amino acids 1-33

**Transmembrane domain:**

amino acids 420-442

**N-glycosylation sites.**

amino acids 126-129, 357-360, 496-499, 504-507

**cAMP- and cGMP-dependent protein kinase phosphorylation site.**

amino acids 465-468

**Tyrosine kinase phosphorylation site.**

amino acids 136-142

**N-myristylation sites.**

amino acids 11-16, 33-38, 245-250, 332-337, 497-502, 507-512

## **FIGURE 125**

CCGTTATCGTCTTGCCTACTGCTGAATGTCGTCCCAGGAGGAGGAGGCTTGTCCGCTG  
ACCCAGAGATGGCCCGAGCGAGCAAATTCTACTGTCGGCTGCGCGCTACCGTGGCGAGCT  
AGCAACCTTCCCCTGGATCTCACAAAACTCGACTCCAAATGCAAGGAGAAGCAGCTTGTCT  
GGTTGGGAGACGGTGAAGAGAATCTGCCCCCTATAGGGGAATGGTGCACAGCCCTAGGGATC  
ATTGAAGAGGAAGGCTTCTAAAGCTTGGCAAGGAGTGCACACCGCCATTACAGACACGTAGT  
GTATTCTGGAGGTGAATGGTCACATATGAACATCTCCGAGAGGTTGTGTTGGCAAAAGTGAAG  
ATGAGCATTATCCCCTTGGAAATCAGTCATTGGAGGGATGATGGCTGGTGTATTGGCAGTT  
TTAGCCAATCCAACTGACCTAGTGAAGGTTCAGATGCAAATGGAAGGAAAAGGAAACTGGAAGG  
AAAACCATTGCGATTCGATTCGTTGACATCATGCATTGCAAAATCTAGCTGAAGGAGGAATAC  
GAGGGCTTGGCAGGCTGGTACCCAAATATACAAAGAGCAGCACTGGTGAATATGGGAGATTAA  
ACCACTTATGATAACAGTGAAACACTACTTGGTATTGAATACACCACCTGAGGACAATATCATGAC  
TCACGGTTATCAAGTTATGTTCTGGACTGGTAGCTCTATTCTGGAACACCAGCCATGTCA  
TCAAAAGCAGAATAATGAATCAACCACGAGATAAACAAAGGAAGGGACTTTGTATAAATCATCG  
ACTGACTGCTGATTCAGGCTGTTCAAGGTGAAGGATTCAATGAGTCTATATAAAGGCTTTTACC  
ATCTTGGCTGAGAATGACCCCTGGTCAATGGTGTCTGGCTTACTTATGAAAAAATCAGAGAGA  
TGAGTGGAGTCAGTCATTTTAA

## **FIGURE 126**

MSVPEEEEERLLPLTQRWPRASKFLLSGCAATVAELATFPLDLTKTRLQMGEAALARLGDGARES  
APYRGMVRTALGIIEEEGFLKLWQGVTPAIYRHVVYSGGRMVTYEHLREVVFGKSEDEHYPLWKS  
VIGGMMAGVIGQFLANPTDLVKVQMOMEGRKLEGKPLRFRGVHHAFAKILAEGGIRGLWAGWVP  
NIQRAALVNMGDLTYDTVKHYLVNTPLEDNIMTHGLSSLCGGLVASILGTPADVIKSrimnQP  
RDKQGRGLLYKSSTDCLIQAVQGEGFMSLYKGFLPSWLRMTPWSMVFWLTYEKIREMSGVSPF

**Transmembrane domains:**

amino acids 25-38, 130-147, 233-248

## **FIGURE 127**

CGCGGATCGGACCCAAGCAGGTGGCGGCGGCGAGGAGAGCGGGCGGTAGCTCCTCGAC  
CCCCGTGTCGGGCTAGTCCAGCGAGGCGACGGGCGGTGGCCATGCCAGGCCGGCATGG  
AGCGGTGGCGCGACCGGCTGGCGTGGTACGGGGGCTCGGGGGCATGGCGCGGTGGCC  
CGGGCCCTGGTCCAGCAGGGACTGAAGGTGGTGGCTGCGCCGCACTGTGGCAACATCGAGGA  
GCTGGCTGCTGAATGTAAGAGTCAGGCTACCCCAGGACTTGTACCCCTACAGATGTGACCTAT  
CAAATGAAGAGGACATCCTCTCCATGTTCTCAGCTATCCGTTCTCAGCACAGCGGTGAGACATC  
TGCATCAACAATGCTGGCTTGGCCGGCCTGACACCCCTGCTCAGGCAGCACCGACTGGTGGAA  
GGACATGTTCAATGTGAACGTGCTGGCCCTCAGCATCTGCACACGGAAAGCCTACCAGTCCATGA  
AGGAGCGGAATGTGGACGATGGGACATCATTAACATCAATAGCATGTCGGCCACCGAGTGTGTTA  
CCCCTGTCGTGACCCACTCTATAGGCCACCAAGTATGCCGTACTGCGCTGACAGAGGGACT  
GAGGCAAGAGCTCGGGAGGCCAGACCCACATCCGAGCCACGTGCATCTCTCAGGTGTGGTGG  
AGACACAATTGCCCTCAAACCTCACGACAAGGACCTGAGAAGGCAGCTGCCACCTATGAGCAA  
ATGAAGTGTCTCAAACCCGAGGATGTGGCCGAGGCTTTACGGTCTCAGCACCCCCCGACA  
CATCCAGATTGGAGACATCCAGATGAGGCCACGGAGCAGGTGACCTAGTGACTGTGGGAGCTCC  
TCCTTCCCTCCCCACCCCTCATGGCTGCCCTGCCCTGGATTAGGTGTTGATTCTGGAT  
CACGGGATACCACTCCTGTCCACACCCCGACCAGGGCTAGAAAATTGTTGAGATTTTATA  
TCATCTGTCAAATTGCTTCAGTTGAAATGTGAAAAATGGCTGGGAAAGGAGGTGGTGTCCC  
TAATTGTTTACTTGTAACTTGTCTTGCCCCCTGGGACTTGGCCTTGTCTGCTCTCAGTG  
TCTTCCCTTGACATGGAAAGGAGTTGGCCAAAATCCCCATCTTGTGCACCTCAACGTCTG  
TGGCTAGGGCTGGGTGGCAGAGGGAGGCCACCTTATATCTGTTGTTATCCAGGGCTCC  
AGACTCCCTCCTGCCTGCCACTGCACCCCTCTCCCTTATCTATCTCCTCTCGGCTCCCC  
AGCCCGACTTGGCTTCTTGCCCCCTGGGTACCCCTCCACTGACTCTGACTATGGCAG  
CAGAACACCAGGGCTGGCCAGTGGATTTCATGGTGATCATTAAAAAGAAAAATCGAACCAA  
AAAAAAAAAA

## **FIGURE 128**

MARPGMERWRDRLALVTGASGGIGAAVARALVQQGLKVVGCARTVGNIEELAAECKSAGYPGTLI  
PYRCDLSNEEDIISMFSAIRSQHSGVDICINNAGLARPDTLLSGSTSGWKDMFNVNLALSICTR  
EAYQSMKERNVDDGHIININMSGHRVLPLSVTHFYSATKYAVTALTEGLRQELREAQTHIRATC  
ISPGVVETQFAFKLHDKDPEKAAATYEQMKCLKPEDVAEAVIYVLSTPAHIQIGDIQMRPTEQVT

**Important features of the protein:**

**Signal peptide:**

amino acids 1-17

**N-myristoylation sites.**

amino acids 18-24, 21-27, 22-28, 24-30, 40-46, 90-96, 109-115,  
199-205

**Short-chain alcohol dehydrogenase.**

amino acids 30-42, 104-114

## **FIGURE 129**

AACTTCTACATGGGCCTCCTGCTGCTGGTGCCTTCCTCAGCCTCCTGCCGGTGGCCTACACCAT  
CATGTCCCTCCCACCCCTTGACTGCGGGCCGTCAGGTGCAGAGTCTCAGTGGCCGGAGC  
ACCTCCCTCCCGAGGCAGTCTGCTCAGAGGGCCTGCCAGAATCCAGTTCTGGTTCATGC  
CAGCCTGTAAAAGGCCATGGAACTTGGGTGAATCACCATTAAGAGGGTTTCTGCCA  
GGATGGAAATGTTAGGTCGTTTGTGTCTGCGTGTTCATTCCAGTAGCCACCAGCCACCTGTGG  
CCGTTGAGTGCTTGAAATGAGGAACTGAGAAATTAATTCCATGTATTTTCTCATTTTTA  
TTTAATTTTTAACTGATAGTTGACATATTTGGGGTACATGTGATATTTGGATACATGTTACAA  
TATTATGATCAAATCAGGGTAACTGGGGATATCCCATCACATCAAACATTTATTTTTATTCTT  
TTTAGACAGAGTCTCACTCTGTCACCCAGGGCTGGAGTGCAGTGGGTGCCATCTCAGCTTACTGCAAC  
CTCTGCCTGCCAGGTCAAGCGATTCCATGCCTCCACCTCCAAAGTAGCTGGACTACAGGGCAT  
GCACCACAATGCCCAACTAATTTTTGATTTTTAGTAGAGACGGGTTTTGCCATGTGCCCAGG  
CTGGCCTGAACTCCTGGCCTCAAACAATCCACTTCGCCCTCCAAAGGTTATGATTACA  
GGCGTGAGCCACCGCTGGCTAAACATTTATTTTGTTTTGGAACTTTGAAATTT  
ACAATGAATTTTGTTAACTGTCATCTCCCTGCTGCTTGGAACACTGGACTTCTCCCT  
ATCTAACTGTAATTTGTACCAGTTAACCAACCGTACTTCATCCCCACCTCTCTTATCCTTCC  
AACCTTGATCACCTCATTCTACTCTACCTCCATGAGACTCCACTTTTTAGCTCCACATGTG  
AGTAAGAAATGCAATTTGCTTTCTGCTGGCTTTTTCACTTAACATAATGACTCCCT  
TTCCATCCATGTGTGCTGCAATGACAGGGATTCGTTCTAATTCAATTAAAAATACCACACATG  
GCAAAAA

## **FIGURE 130**

MGLLLLVLFLSLLPVAYTIMSLPPSFDCGPFRCRVSVAREHLPSPRGSSLRGPRPRIPVLVSCQPV  
KGHGTLGESPMFKRVFCQDGTVRSFCVCAVHFSSHQPPVAVECLK

**Important features of the protein:**

**Signal peptide:**

amino acids 1-18

**N-myristoylation site.**

amino acids 86-92

**Zinc carboxypeptidases, zinc-binding region 2 signature.**

amino acids 68-79

## **FIGURE 131**

TTCTGAAGTAACGGAAGCTACCTTGATAAAGACCTAACACTGCTGACCATGATCAGCGCAGCCTGGAGC  
ATCTTCCTCATCGGGACTAAATTGGGCTGTCCTCAAGTAGCACCTCTATCAGTTATGGCTAAATCCCTG  
TCCATCTGTGTCGCGATGGGGTTTCATTTACTGTAATGATCGCTTCTGACATCCATTCCAACAG  
GAATACCAGAGGATGCTACAACTCTACCTTCAGAACACAAATAATAATGCTGGATTCCCTCAGAT  
TTGAAAAACTTGCTGAAAGTAGAAAGAATATAACCTATACCAACAGTTAGATGAATTCCCTACCAACCT  
CCCAAAGTATGTAAGAGTATCATTGCAAGAAAATAACATAAGGACTATCACTTATGATTCACTTCAA  
AAATTCCCTATCTGGAAGAATTACATTAGATGACAACCTGTCTCTGCAGTTAGCATAGAAGAGGGAGCA  
TTCGAGACAGCAACTATCTCGACTGCTTTCTGTCGGTAATCACCTAGCACAATTCCCTGGGTTT  
GCCAGGACTATAGAAGAACTACGCTGGATGATAATCGCATATCCACTATTCATCACCATCTCTTCAA  
GTCTCACTAGTCTAAACGCTGGTCTAGATGAAACCTGTTGAACAATCATGGTTAGGTGACAAGATT  
TTCTTCACCTAGTTAATTGACAGAGCTGTCCTGGTGCAGAATTCCCTGACTGCTGACCAAGTAAACCT  
TCCAGGCACAAACCTGAGGAAGCTTATCTCAAGATAACCACATCAATCGGGTGCCTTAAATGCTTTT  
CTTATCTAAGGCAGCTCTATGACTGGATATGTCATAATAACCTAAGTAATTACCTCAGGGTATCTT  
GATGATTGGACAATATAACACAACGATTCTCGAACAAATCCCTGGTATTGGGGTCAAGATGAAATG  
GGTACGTGACTGGTTACAATCACTACCTGTGAAGGTCAACGTGCGTGGGCTCATGTGCCAACCCCCAGAAA  
AGGTTGGTGGGATGGCTATTAGGATCTCAATGCAGAACTGTTGATTGTAAGGACAGTGGGATTGTAAGC  
ACCATTCAAGATAACCACGTCAAAACCAACACAGTGTATCCGCCAACGGACAGTGGCCAGCTCCAGTGAC  
CAAACAGCCAGATAATAAGAACCCAAGCTCACTAAGGATCAACAAACCAACAGGGAGTCCCTCAAGAAAAAA  
CAATTACAATTACTGTGAAGTGTGACCTCTGATACCATTCTATCTCTGGAAACTGCTCTACCTATG  
ACTGCTTGAGACTCAGCTGCCCTAAACTGGCCATAGCCCCGATTTGGATCTATAACAGAAACAATTGT  
AACAGGGAAACGCAGTGAGTACTGGTCACAGCCCTGGAGCCTGATTGACCTTATAAAAGTATGCATGGT  
CCATGGAAACCAACCTCTACCTTATTTGATGAAACTCCTGTTGATTGAGACTGAAACTGCACCCCTT  
CGAATGTACAACCCCTACAACCACCCCTCAATCGAGAGCAAGAGAAAGAACCTTACAAAACCCAATTAC  
TTTGGCTGCCATCTGGTGGGGCTGTGGCCCTGGTACCTGCTTGTGTTAGTGTGTTGGTATG  
TTCATAGGAATGGATCGCTTCTCAAGGAACGTGTCATATAGCAAAGGGAGGAGAAGAAAGGATGACTAT  
GCAGAACGCTGGCACTAAGAAGGACAACCTATCCTGGAAATCAGGAAACTCTTCAAGATGTTACCAAT  
AAGCAATGAACCCATCTGAAGGAGGAGTTGTAATACACACCATACTTCTCCTAATGGAATGAATCTGT  
ACAAAACAAATCACAGTGAAGGAGCTAGTAACCGAAGCTACAGAGACAGTGGTATTCCAGACTCAGATCAC  
TCACACTCATGATGCTGAAGGACTCACAGCAGACTTGTGTTGGTTTTAACCTAAGGGAGGTGATG  
GT

## **FIGURE 132**

MISAAWSIFLIGTKIGLFLQVAPLSVMAKSCPSVCRC DAGFIYCNDRFLTSIPTGIPEDATTLYL  
QNNQINNAGIPSDLKNLLKVERIYLYHNSLDEFPTNLPKYVKELHLQENNIRTITYDSLSKIPYL  
EELHLDNSVSAVSTIEEGAFRDSNYLRLFLSRNHLSI PWGLPRTIEELRLDDNRISTISSPSL  
QGLTSLKRLVLDGNLNNHGLGDKVFFNLVNLTELSLVRNSLTAAPVNLPGTNLRKLYLQDNHIN  
RVPPNAFSYLRQLYRLDMSNNNLSNLPQGIFDDLDNITQLILRNNPWYCGCKMKWV RDWLQSLPV  
KVNVRGILMCQAPEKVRGMAIKDLNAELFDCKDSGIVSTIQTIAPI PNTVYPAQGQWPAPVTKQPD  
IKNPKLTKDQQTTGSPSRKTITITVKSVTSDTIHISWKLALPMTALRLSWLKLGHSPAFGSITET  
IVTGERSEYLVTALEPDSPYKVCVPMETSNLYLFDETPVCIETETAPLRMYNPTTLNREQEKE  
PYKNPNLPLAAIIGGAVALVTIALLALVCWYVHRNGSLFSRNCAYSKGRRKDDYAEAGTKK DNS  
ILEIRETSFQMLPISNEPISKEEVIHTIFPPNGMNLKNNHSESSSNRSYRDSGIPDSDHSHS

**Important features of the protein:**

**Signal peptide:**

amino acids 1-28

**Transmembrane domain:**

amino acids 531-552

**N-glycosylation sites.**

amino acids 226-229, 282-285, 296-299, 555-558, 626-629, 633-636

**Tyrosine kinase phosphorylation site.**

amino acids 515-522

**N-myristoylation sites.**

amino acids 12-17, 172-177, 208-213, 359-364, 534-539, 556-561, 640-645

**Amidation site.**

amino acids 567-570

**Leucine zipper pattern.**

amino acids 159-180

**Phospholipase A2 aspartic acid active site.**

amino acids 34-44

### **FIGURE 133**

CCGTCACTCCCCCTGCAGCCACCCCTCCCAGAGTCCTTGCCCAGGCCACCCAGGCTTCTGGCA  
GCCCTGCCGGGCCACTTGTCTTCATGTCTGCCAGGGGGAGGTGGGAAGGAGGTGGGAGGAGGGCG  
TGCAGAGGGCAGTCTGGCTGGCCAGAGCTCAGGGTGTGAGCGTGTGACCAGCAGTGAGCAGAG  
GCCGGCCATGGCCAGCCTGGGCTGCTCCTGCTCTTAACAGCAGTGCACCCGCTGTGGT  
CCTCCTCACTGCCTGGGCTGGACACTGCTGAAAGTAAAGCCACCAATTGAGACCTGATCCTGTCT  
GCGCTGGAGAGAGGCCACCGTCTCCTAGAACAGAGGCTGCCTGAAATCAACCTGGATGGCATGGT  
GGGGGTCCGAGTGTGGAAAGAGCAGCTAAAAAGTGTCCGGAGAAGTGGGCCAGGAGGCCCTGC  
TGCAGCCGCTGAGCCTGCGCGTGGGATGCTGGGGAGAAGCTGGAGGCTGCCATCCAGAGATCC  
CTCCACTACCTCAAGCTGAGTGTGATCCAAGTACCTAACAGAGGAGTCCAGCTGACCCCTCCAGGCCGG  
GTTTTGGAAGCTCCCACATGCCCTGGATCCACACTGATGCCCTTGGTGTACCCCACGTTGGGC  
CCCAGGACTCATTCTCAGAGGAGAGAAGTGAAGTGTGCCCTGGTGCAGCTGCTGGAAACCGGGACG  
GACAGCAGCGAGCCCTGCCCTCAGACCTCTGCAGGAGCCTCATGACCAAGCCGGCTGCTC  
AGGCTACTGCCCTGCCACCAACTGCTCTCCTCTGGCCAGAATGAGGGATGCACACAGG  
GACCACTCAACAGAGCCAGGACTATATCAACCTCTTCTGCGCCAACATGATGGACTTGAACCGC  
AGAGCTGAGGCCATCGGATACGCCAACCTACCCGGACATCTCATGGAAAACATCATGTTCTG  
TGGAATGGCGGCTCTCGACTTCTACAAGCTCCGGTGGCTGGAGGCCATTCTCAGCTGGCAGA  
AACAGCAGGAAGGATGCTCGGGAGCCTGATGCTGAAGATGAAGAATTATCTAAAGCTATTCAA  
TATCAGCAGCATTTCGAGGAGAGTGAAGAGGCGAGAAAACAATTCCAGATTCTCGCTCTG  
TGCTCAGGCTGGAGTACAGTGGCGCAATCTGGCTCACTGCAACCTTGCCTCTGGTTCAAGC  
AATTCTCTGCCCTACCTCCGAGTAGCTGGACTACAGGAGCGTGCACCCATACCTGGCTAAT  
TTTATATTTTTAGTAGAGACAGGGTTCATCATGTTGCTCATGCTGGTCTCGAAGTCCCTGAT  
CTCAAGAGATCCGCCACCTCAGGCTCCCAAAGTGTGGATTTAGGTGTGAGCCACCCTGTCTG  
GCTGAAAAGCACTTCAAAGAGACTGTGTGAATAAAGGGCAAGGTTCTGCCACCCAGCACTC  
ATGGGGCTCTCCCTAGATGGCTGCTCCTCCACAAACACAGCCACAGCAGTGGCAGCCCTGG  
GTGGCTCCTATACATCCTGGCAGAATACCCCCCAGCAAACAGAGAGCCACACCCATCCACACCG  
CCACCAAGCAGCGCTGAGACGGACGGTCCATGCCAGCTGCCCTGGAGGAGGAACAGACCC  
TTAGTCCTCATCCCTAGATCCTGGAGGGCACGGATCACATCCTGGAGAAGAGGCATCTGGAGG  
ATAAGCAAAGCCACCCGACACCAATCTGGAAGCCCTGAGTAGGCAGGGCAAGGGTAGGTGGG  
GGCCGGGAGGGACCCAGGTGTGAACGGATGAATAAGTCACGCAACTGCAACTGAAACAAAAAAA

## **FIGURE 134**

MSARGRWEGGRRACRGSGLARAQGAERVTSSEQRPMASLGLLLLLTLAPPLWSSSLPGLD  
TAESKATIADLILSALERATVFQRLPEINLDGMGVVRVLEEQLKSVREKWAQEPLLQPLSLRV  
GMLGEKLEAAIQRSLHYLKLSDPKYLREFQQLTQPGFWKLPHAWIHTDASLVYPTFGPQDSFSEE  
RSDVCLVQLLGTGTDSEPCGLSDLRSLMTKPGCSGYCLSHQLLFFLWARMRGCTQGPLQQSQD  
YINLFCANMMDLNRAEAIGYAYPTRDIFMENIMFCGMGGFSDFYKLRWLEAILSWQKQQEGCFG  
EPDAEDEELSKAIQYQQHFSRRVKRREKQFPDSRSVAQAGVQWRNLGSLOPLPPGFQFSCLILP  
SSWDYRSVPYPLANFYIFLVETGFHHVAHAGLELLISRDPPTSGSQVGL

**Important features of the protein:**

**Signal peptide:**

amino acids 1-26

**Transmembrane domain:**

amino acids 39-56

**Tyrosine kinase phosphorylation sites.**

amino acids 149-156, 274-282

**N-myristylation sites.**

amino acids 10-16, 20-26, 63-69, 208-214

**Amidation site.**

amino acids 10-14

**Glycoprotein hormones beta chain signature 1.**

amino acids 230-237

### **FIGURE 135**

GGTCTGAGTGCAGAGCTGCTGTCATGGCGGCCGCTCTGTGGGCTTCTTCCGCTGCTGCTG  
CTGCTGCTATCGGGGATGTCCAGAGCTCGAGGTGCCGGGCTGCTGCTGAGGGATCGGAGG  
GAGTGGGGTCGGCATAGGAGATCGCTCAAGATTGAGGGCGTGCAGTTGTTCCAGGGTGAAGC  
CTCAGGACTGGATCTCGCGGCCGAGTGCAGTGGTAGACGGAGAAGAGCACGTCGGTTCTTAAG  
ACAGATGGGAGTTTGTGGTTCATGATATACTTCTGGATCTTATGTAGTGGAAAGTTGTATCTCC  
AGCTTACAGATTTGATCCCGTTGAGTGGATATCACTCGAAAGGAAAATGAGAGCAAGATATG  
TGAATTACATCAAAACATCAGAGGTTGTCAGACTGCCCTATCCTCTCAAATGAAATCTCAGGT  
CCACCTCTTACTTTATTAAAAGGAATCGTGGGCTGGACAGACTTCTAATGAACCCAATGGT  
TATGATGATGGTTCTCCTTATTGATATTGTGCTCTGCCTAAAGTGGTCAACACAAGTGATC  
CTGACATGAGACGGAAATGGAGCAGTCAATGAATATGCTGAATTCCAACCATGAGTTGCCTGAT  
GTTTCTGAGTTCATGACAAGACTCTCTCTCAAATCATCTGCAAATCTAGCAGCGGCAGCAG  
TAAAACAGGCAAAGTGGGCTGGCAAAGGAGGTAGTCAGGCCGTCAGAGCTGGCATTGCAC  
AAACACGGCAACACTGGTGGCATCCAAGTCTGGAAAACCGTGTGAAGCAACTACTATAAATT  
GAGTCATCCCGACGTTGATCTTACAACGTGTATGTT  
AACTTTTAGCACATGTTTGACTTGGTACACGAGAAAACCCAGCTTCATCTTGTCTGTAT  
GAGGTCAATATTGATGTCACTGAATTAATTACAGTGTCTATAGAAAATGCCATTAATAAATTAT  
ATGAACTACTATACTTGTATTAATTAAAACATCTTAATCCAGAAAATCAAAAAAAAAAAAA  
AAAAAAAAAAAAAAA

## **FIGURE 136**

MAAALWGFFPVLLLLLSDVQSSVPGAAEGSGSGVGIGDRFKIEGRAVPGVKPQDWISAA  
RVLVDGEEHVGFLLKTDGSFVVHDIPSGSYVVEVSPAYRFDPVRVDITSKGKMRARYVNYIKTSE  
VVRLPYPLQMKSSTGPPSYFIKRESWGWTDFLMNPMVMMMLPLLIFVLLPKVVNTSDPDMRREME  
QSMNMLNSNHELPDVSEFMTRLFSSKSSGKSSSGSSKTGKSGAGKRR

**Important features of the protein:**

**Signal sequence:**

amino acids 1-23

**Transmembrane domain:**

amino acids 161-182

**N-glycosylation site.**

amino acids 184-187

**Glycosaminoglycan attachment sites.**

amino acids 37-40, 236-239

**cAMP- and cGMP-dependent protein kinase phosphorylation site.**

amino acids 151-154

**N-myristoylation sites.**

amino acids 33-38, 36-41, 38-44, 229-234

**Amidation site.**

amino acids 238-241

**ATP/GTP-binding site motif A (P-loop).**

amino acids 229-236

## **FIGURE 137**

GATGGCGCAGCCACAGCTCTGTGAGATTGATTCTCCCCAGTTCCCTGTGGGTCTGAGGGGA  
CCAGAAGGGT GAGCTACGTTGGCTTCTGAAAGGGGAGGCTATATGCGTCAATTCCCCAAACAA  
GTTTGACATTCCCTGAAATGTCATTCTATCTATTCACTGCAAGTGCTGCTGTTCCAGGC  
CTTACCTGCTGGCACTAACGGCGGAGCCAGGATGGGACAGAATAAGGAGCCACGACCTGTGC  
CACCAACTCGCACTCAGACTCTGAACCTCAGACCTGAAATCTTCTTCACGGGAGGCTGGCAGT  
TTTCTTACTCCTGTGGCTCCAGATTCAAGGCTAAGATGAAAGCCTCTAGTCCTGCCTTCAGC  
CTTCTCTGCTGCGTTTATCCTATGGACTCCTCCACTGGACTGAAGACACTCAATTGGG  
AAGCTGTGTGATGCCACAAACCTCAGGAAATACGAAATGGATTTCTGAGATAACGGGCAGTG  
TGCAAGCCAAGATGAAACATTGACATCAGAATCTAAGGAGGACTGAGTCCTGCAAGACACA  
AAGCCTGCGAATCGATGCTGCCCTGCCATTGCTAAGACTCTATCTGGACAGGGTATTAA  
AAACTACCAGACCCCTGACCATTATACTCTCCGAAGATCAGCAGCCTGCCATTCCCTTCTTA  
CCATCAAGAAGGACCTCCGGCTCTCATGCCACATGACATGCCATTGTGGGAGGAAGCAATG  
AAGAAATACAGCCAGATTGAGTCACTTGAAAAGCTGAAACCTCAGGCAGCAGTGTGAAGGC  
TTTGGGGAACTAGACATTCTCTGCAATGGATGGAGGAGACAGAATAGGAGGAAAGTGATGCTG  
CTGCTAAGAATATTGAGGTCAAGAGCTCAGTCTCAATACCTGCAGAGGAGGCATGCCCAA  
ACCACCATCTCTTACTGTACTAGTCTTGTGCTGGTCACAGTGTATCTTATTTGCTATTG  
CTTCCTTGCATGATTGCTTTATGCATCCCCATCTAATTGAGACCATACTTGATAAGATT  
TGTAATATCTTCTGCTATTGGATATATTATTAGTTAATATATTATTTATTTGCTATT  
ATGTATTATTTTACTGGACATGAAACTTTAAAAAAATTACAGATTATTTATAACCTG  
ACTAGAGCAGGTGATGTATTGATACAGTAAAAAAACCTTGTAAATTCTAGAAGAGTGG  
CTAGGGGGTTATTCAATTGACTAAGGACATATTACTCATGCTGATGCTCTGTGAGAT  
ATTTGAAATTGAACCAATGACTACTTAGGATGGGTGGAATAAGTTTGATGTGGAATTGCAC  
ATCTACCTACAATTACTGACCATCCCCAGTAGACTCCCCAGTCCCATATTGTGATCTCCAG  
CCAGGAATCCTACACGGCCAGCATGTATTCTACAAATAAGTTCTTGCATACCAAAAAAA  
AAAAAA

## **FIGURE 138**

MRQFPKTSFDISPMSFSIYSLQVPAVGLTCWALTAEPGWGQNKGATTCATNSHSDSELRPEIF  
SSREAWQFFLLLWSPDFRPKMKASSLAFSLLSAAFYLLWTPSTGLKTLNLGSCVIATNLQEIRNG  
FSEIRGSVQAKDGNIDIRILRRTESLQDTK PANRCCLRHLLRLYLDdrvFKNYQTPDHYTLRKIS  
SLANSFLTIKKDLRLSHAHMTCHCGEEAMKKYSQILSHFEKLEPQAAVVKALGELDILLQWMEET  
E

**Important features of the protein:**

**Signal peptide:**

amino acids 1-42

**cAMP- and cGMP-dependent protein kinase phosphorylation sites.**

amino acids 192-195, 225-228

**N-myristoylation sites.**

amino acids 42-47, 46-51, 136-141

## **FIGURE 139**

CCTGGAGCCGGAAGCGCGGCTGCAGCAGGGCGAGGCTCCAGGTGGGGTCGGTCCGCATCCAGCC  
TAGCGTGTCCACGATTCCGGCTGGGCTCCGGACTTCGCTACCTGTGGTAGCGATCGAGGTGC  
TAGGGATCGCGGTCTTCCTCGGGGATTCTCCCGGCTCCCGTCTGGAGCCAGTTCAACTGGACCCACGCTGCC  
CACGGAGCGGAGCCCCCAGCGCCGAACCCCTCGGCTGGAGCCAGTTCAACTGGACCCACGCTGCC  
ACCACCTCTCTCAGTAAAGTTTATTGTCTGATAGATGCCTTGAGAGATGATTGTGTTG  
GGTCAAAGGGTGTGAAATTATGCCCTACACAACCTACAGTTACTATGCCCTGAATCAAGGATTGATGACGGGGAG  
CCTTCCTGGCTTGTGACGTCATCAGGAACCTCAATTCTCCTGCACTGCTGGAGACAGTGTGA  
TAAGACAAGCAAAGCAGCTGGAAAAGAAATAGTCTTTATGGAGATGAAACCTGGGTTAAATTA  
TTCCCAAAGCATTGTGGAATATGATGGAACAACCTCATTTCGTCAGATTACACAGAGGT  
GGATAATAATGTACGAGGCATTGGATAAAGTATTAAAAAGAGGGAGTTGGACATATTAATCC  
TCCACTACCTGGGGCTGGACCACATTGGCACATTTCAGGGCCAAACAGCCCCCTGATTGGGAG  
AAGCTGAGCGAGATGGACAGCGTGTGATGAAGATCCACACCTCACTGCACTGAGTCAGAGAGAGA  
GACGCCCTTACCCAAATTGCTGGTTCTTGCTGGTACCATGGCATGTCAGAAACAGGAAGTCACG  
GGGCCTCCTCCACCGAGGAGGTGAATACACCTCTGATTAAATCAGTTCTGCGTTGAAAGGAAA  
CCCGGTGATATCCGACATCCAAGCACGTCCAATAGACGGATGTGGCTGCACACTGGCAGTAGC  
ACTTGGCTTACCGATTCCAAAAGACAGTGTAGGGAGCCTCTATTCCAGTTGTGGAAGGAAGAC  
CAATGAGAGAGCAGTTGAGATTTCACATTGAATACAGTGCAGCTAGTAAACTGTTGCAAGAG  
AATGTGCCGTATGAAAAAGATCCTGGTTGAGCAGTTAAATGTCAGAAAGATTGCATGG  
GAACGTGATCAGACTGTACTTGAGGAAAAGCATTCAAGAGTCTATTCAACCTGGCTCCAAGG  
TTCTCAGGCAGTACCTGGATGCTCTGAAAGACGCTGAGCTTGTCCCTGAGTGCACAGTGGCCAG  
TTCTCACCCCTGCTCTGCTCACCGTCCCACAGGCACTGCACAGAAAGGCTGAGCTGGAAAGTCCA  
CTGTCATCTCCTGGTTTCTGCTTTTATTGGTACCTCTGGTCTTTCTGGCCGTTACGT  
CATTGTGTGACCTCAGCTGAAAGTTCGTCGACTTCTGTGGCCTCTCGTGGCTGGCGGAGGCT  
GCCTTCGTTTACCAAGACTCTGGTTGAACACCTGGTGTGCAAGTGTGCTGGCAGTGCCTGGAC  
AGGGGGCTCAGGGAAAGGACGTGGAGCAGCTTATCCCAGGCCTCTGGGTGTCGGACACAGGTG  
TTCACATCTGCTGTCAGGTCAAGTCAGATGCCCTCAGTTCTGGAAAGCTAGGTTCTGGACTGTAC  
CAAGGTATTGTAAGAGCTGGGGTACAGAGGAACAAGGCCCCCAGCTGAGGGGGTGTGAA  
TCGGACAGCCTCCCAGCAGAGGTGTGGAGCTGAGCTGAGGGAAAGAGAGACAATGCCCTGG  
CACTCAGGAGGGTCAAAGGAGACTTGGTCGACCAACTCATCTGCCACCCCCAGAATGCATCCT  
GCCTCATCAGGTCCAGATTCTTCCAAGGGGAGCTTCTGTTGAAATTCTTAGTCTTGGCC  
TCGGACACCTCATTGTTAGCTGGGAGTGGTGGTGAGGGCAGTGAAGAAGAGGCGGATGGTCAC  
ACTCAGATCCACAGAGGCCAGGATCAAGGGACCCACTGCAGTGGCAGCAGGACTGTGGCCCC  
ACCCCAACCCCTGCACAGCCCTCATCCCTCTGGCTGAGCCGTGAGGGCCCTGTGCTGAGTGT  
CTGACCGAGACACTCACAGCTTGTCACTAGGGCACAGGCTTCCCTGGAGCCAGGATGATCTGTG  
CCACGCTTGCACCTCGGGCCATCTGGGCTCATGCTCTCTCCTGCTATTGAATTAGTACCTAG  
CTGCACACAGTATGTAGTTACCAAAAGAATAAACGGCAATAATTGAGAAAAAAA

## **FIGURE 140**

MRLGSGTFATCCVAIEVLGIAVFLRGFFPAPVRSSARAEHGAEPPEPSAGASSNWTLLPPPLF  
SKVVVILIDALRDDFVFGSKGVKFMPYTTYLVKGASHSFVAEAKPPTVTMPRIKALMTGSLPGF  
VDVIRNLNSPALLEDSVIRQAKAAGKRIVFYGDETWVKLFPKHFVEYDGTTFFFSDYTEVDNNV  
TRHLDKVLKRGDWDILILHYLGLDHIGHISGPNSPLIGQKLSEMDSVLMKIHTSLQSKERETPLP  
NLLVLCGDHGMSETGSHGASSTEEVNTPLILISSAFERKPGDIRHPKHQ

**Important features of the protein:**

**Signal peptide:**

amino acids 1-34

**Transmembrane domain:**

amino acids 58-76

**N-glycosylation sites.**

amino acids 56-60, 194-198

**N-myristoylation sites.**

amino acids 6-12, 52-58, 100-106, 125-131, 233-239, 270-276,  
275-281, 278-284

**Amidation site.**

amino acids 154-158

**Cell attachment sequence.**

amino acids 205-208

## **FIGURE 141**

GGCACGAGGCAAGCCTCCAGTTATCGTACGCACCTGAAAGTCTGAGAGCTACTGCCCTACA  
GAAAGTTACTAGTGCCCTAAAGCTGGCGTGGCACTGATGTTACTGCTGCTGTTGGAGTACA  
ACT  
TCCCTATAGAAAACA  
CTGCCAGCACCTTAAGACCA  
CTCACACCTTCAGAGTGAAGAACTTAAAC  
CCGAAGAAATT  
CAGCATT  
CATGACCAGGATCACAAAGTACTGGTCTGGACTCTGGGAATCTCAT  
AGCAGTTCCAGATA  
AAAAACTACATACGCCAGAGATCTTCTTGCTTGCATTAGCCTCATCCTTGAGCT  
CAGCCTCTGCGGAGAAAGGAAGTCCGATTCTCCTGGGGTCTCTAAAGGGAGTTTGCTCTAC  
TGTGACAAGGATA

## **FIGURE 142**

MLLLLLEYNFPIENNQHLKTTHTFRVKNLNPKKFSIHQDHKVLVLDGNLIAVPDKNYIRPEI  
FFALASSLSSASAEGSPILLGVSKGEFCLYCDKDKGQSHPSLQLKEKLMKLAQKESARRPFI  
FYRAQVGSWNMLESAAHPGWFICTSCNCNEPGVTDKFENRKHIEFSFQPVCKAEMSPSEVSD

**cAMP- and cGMP-dependent protein kinase phosphorylation site.**

amino acids 33-36

**N-myristoylation site.**

amino acids 50-55, 87-92

**Interleukin-1**

amino acids 37-182

## **FIGURE 143**

CTAGAGAGTATAGGCAGAAGGATGGCAGATGAGTGACTCCACATCCAGAGCTGCCCTCCCTTAA  
TCCAGGATCCTGCTCTCCCTGCTCTGTAGGAGTGCCTGTTGCCAGTGTGGGTGAGACAAGTTG  
TCCCACAGGGCTGTCTGAGCAGATAAGATTAAGGGCTGGGTCTGTGCTCAATTAACTCCTGTGG  
CACGGGGCTGGGAAGAGCAAAGTCAGCGGTGCCTACAGTCAGCACCATGCTGGCCTGCCGTGG  
AAGGGAGGTCTGTCTGGCGCTGCTGCTGCTCTCTTAGGCTCCCAGATCCTGCTGATCTATGC  
CTGGCATTTCACGAGCAAAGGGACTGTGATGAACACAATGTCATGGCTCGTTACCTCCCTGCCA  
CAGTGGAGTTGCTGTCCACACATTCAACCAACAGAGCAAGGACTACTATGCCTACAGACTGGG  
CACATCTGAATTCTGGAAGGAGCAGGTGGAGTCCAAGACTGTATTCTCAATGGAGCTACTGCT  
GGGGAGAACTAGGTGTGGAAATTGAAAGACGACATTGACAACGCCATTCCAAGAAAGCACAG  
AGCTGAACAATACTTCACCTGCTTCTCACCATCAGCACCCAGGCCCTGGATGACTCAGTTCAGC  
CTCCTGAACAAGACCTGCTTGGAGGGATTCCACTTGAGTGAAACCCACTCACAGGCTGTCCATGT  
GCTGCTCCACATTCCGTGGACATCAGCACTACTCTCCTGAGGACTCTCAGTGGCTGAGCAGCT  
TTGGACTTGTGTTATCCTATTGATGTGTTGAGATCTCAGATCAGTGTAGTTAGAAAATCC  
ACACATCTTGAGCCTAATCATGTAGTGTAGATCATTAAACATCAGCATTAAAGAAAAAAAAAAA  
AAAAA

## **FIGURE 144**

MLGLPWKGGLSWALLLLLLGSQILLIYAWHFHEQRDCDEHNVMARYLPATVEFAVHTFNQQSKDY  
YAYRLGHILNSWKEQVESKTVFSMELLGRTRCGKFEDDIDNCHFQESTELNNTFTCFFTISTRP  
WMTQFSLLNKTCLEGFH

**Important features of the protein:**

**Signal peptide:**

amino acids 1-25

**N-glycosylation sites.**

amino acids 117-121, 139-143

**N-myristoylation site.**

amino acids 9-15

## **FIGURE 145**

CTGTGCAGCTCGAGGCTCCAGAGGCACACTCCAGAGAGAGCAAGGTTCTGACGCG**GATGAGGAAG**  
CACCTGAGCTGGTGGCTGGCCACTGTCTGCATGCTGCTCTTCAGCCACCTCTGCGGTCCA  
GACGAGGGGCATCAAGCACAGAATCAAGTGGAACCGGAAGGCCCTGCCAGCAGCTGCCAGATCA  
CTGAGGCCAGGTGGCTGAGAACCGCCGGAGCCTCATCAAGCAAGGCCGCAAGCTGACATT  
GACTTCGGAGGCCAGGGCAACAGGTACTACAGGCCAACTACTGGCAGTTCCCAGTGGCATCCA  
CTACAAACGGCTGCTCTGAGGCTAATGTGACCAAGGAGGCATTGTACCGGCTGCATCAATGCCA  
CCCAGGGGGCGAACCCAGGGGGAGTCCAGAAGCCAGACAACAAGCTCCACCAGCAGGTGCTCTGG  
CGGCTGGTCCAGGAGCTTGCTCCCTCAAGCATTGCGAGTTTGGTGGAGAGGGCGCAGGACT  
TCGGGTACCATGCACCAGCCAGTGCCTCTGCCTCTGGCTTGATCTGGCTATGGTGA**AAT**  
**AAG**CTTGCCAGGAGGCTGGCAGTACAGAGGCCAGCAGCAGCAAATCTGGCAAGTGACCCAGCT  
CTTCTCCCCAAACCCACGCGTGTCTGAAGGTGCCAGGAGCGGCCATGCACTCGCACTGCAAA  
TGCGCTCCCACGTATGCGCCCTGGTATGTGCCTGCGTTCTGATAGATGGGGACTGTGGCTCT  
CCGTCACTCCATTCTCAGCCCTAGCAGAGCGTCTGGCACACTAGATTAGTAGTAAATGCTTGAT  
GAGAAGAACACATCAGGCACTGCGCCACCTGCTCACAGTACTTCCAACAACTCTAGAGGTAG  
GTGTATTCCGTTTACAGATAAGGAAACTGAGGCCAGAGAGCTGAAGTACTGCACCCAGCATC  
ACCAGCTAGAAAGTGGCAGAGCCAGGATTCAACCCCTGGTTGTCTAACCCAGGTTTCTGCTCT  
GTCCAATTCCAGAGCTGTCTGGTGA~~TCA~~TTATGTCTCACAGGGACCCACATCAAACATGTAT  
CTCTAA~~T~~GTGAAAGCTCCATGTTAGAAATAATGAAAACACCTGA

## **FIGURE 146**

MRKHLSWWLATVCMLLFSHLSAVQTRGIKHRIKWRKALPSTAQITEAQVAENRPGAFIKQGRK  
LDIDFGAEGNRYYEANYWQFPDGIHYNGCSEANVTKEAFVTGCINATQAANQGEFQKPDNLHQO  
VLWRLVQELCSLKHCFWLERGAGLRVTMHQPVLLCLLALIWLMVK

**Important features of the protein:**

**Signal peptide:**

amino acids 1-26

**Transmembrane domain:**

amino acids 157-171

**N-glycosylation sites.**

amino acids 98-102, 110-114

**Tyrosine kinase phosphorylation site.**

amino acids 76-83

**N-myristoylation sites.**

amino acids 71-77, 88-94, 93-99, 107-113, 154-160

**Amidation site.**

amino acids 62-66

## **FIGURE 147**

GCCTTGGCCTCCAAAGGGCTGGGATTATAGCGTGACCAACATGCTGGTCCAGAGTCTCATT  
CCTGATGATTTATAGACTCAAAGAAAACTCATGTTCAGAAGCTCTCTCTGGCCTCCTCT  
CTGTCTTCTTCCCTCTTCTTCTTAAATTAGTAGCATCTACTCAGAGTCATGCAAGCTGG  
AAATCTTCATTTGCTTGTCAAGGGTAGGTCACTGAGTCTAGTTTATTGGAAATTT  
CAACTTCAGATTCAAGGGGTACATGTGAAGGTTGTTATGAGTATATTGCATGATGCTGAGG  
TTTGGGGT

## **FIGURE 148**

MFRSSLLFWPPLCLLSLFLLILISSIYSESCKLEIFHFACQWGRSLSLSFYFLKFQLSDSGGTCE  
GLFYEYIA

**Important features of the protein:**

**Signal peptide:**

amino acids 1-25

**N-myristoylation site.**

amino acids 62-68

## **FIGURE 149**

GTCTCCGCGTCACAGGAACCTTCAGCACCCACAGGGCGGACAGCGCTCCCTCTACCTGGAGACTTGAC  
TCCCGCGCGCCCAACCTGCTTATCCCTTGACCGTCAGAGATCCTGCAGCCGCCAGTCC  
CGGCCCCCTCTCCCGCCCCACACCCACCCCTCTGGCTCTCCTGTTTACTCCTCCTTTCAATTATA  
ACAAAAGCTACAGCTCCAGGAGCCAGCGCCGGCTGTGACCCAAGCCGAGCGTGGAAGAATGGGTT  
CCTCGGGACCGGCACCTGGATTCTGGTGTAGGCTCCGATTCAAGCTTCCCCAACCTGGAGGAA  
GCCAAGACAAATCTCTACATAATAGAGAATTAAGTCAGAAAAGACCTTGAATGAACAGATTGCTGAA  
GCAGAAGAAGACAAGATTAAAAAAACATATCCTCCAGAAAACAAGCCAGGTCAAGAGCAACTATTCTT  
TGTGATAACTGAACTGCTAAAGGCAATAACAGAAAAGGAAAAATTGAGAAAGAAAGACAATCTA  
TAAGAAGCTCCCCACTTGATAATAAGTTGAATGTGGAGATGTTGATTCAACCAAGAATCGAAAATCG  
ATCGATGATTATGACTCTACTAAGAGTGGATTGGATCATAAATTCAAGATGATCCAGATGGTCTTC  
TCAACTAGACGGACTCCTTAACCGCTGAAGACATTGTCATAAAATCGCTGCCAGGATTATGAAG  
AAAATGACAGAGCCGTGTTGACAAGATTGTTCTAAACTACTTAATCTCGGCCTTATCACAGAAC  
CAAGCACATACACTGGAAGATGAAGTAGCAGAGGTTTACAAAAAATTAAATCTCAAAGGAAGCCAACAA  
TTATGAGGAGGATCCAATAAGCCCACAAGCTGGACTGAGAATCAGGCTGGAAAAATACCAGAGAAAG  
TGACTCCAATGGCAGCAATTCAAGATGGTCTGCTAAGGGAGAAAACGATGAAACAGTATCTAACACA  
TTAACCTTGACAAATGGCTGGAAAGGAGAACTAAACCTACAGTGAAGACAACTTGAGGAACCTCA  
ATATTCCCAAATTCTATGCGCTACTGAAAAGTATTGATTGAGAATGATGGTGAACATGAGAA  
CACTGATTACTATCATGAAAACACTGATTGACTTTGTGAAGATGATGGTGAACATGAGAA  
CCAGAAGAAGGTGTTCTACCTGAAAAGTGGATGAAATGATTGCTCTCAGACCAAAAACAAGT  
AGAAAAAAATGCTACTGACAATATAAGCAAGCTTCCAGCACCACAGAGAGTCATGAAGAAA  
CAGACAGTACCAAGGAAGAAGCAGCTAAGATGGAAAAGGAATATGGAAGCTTGAAGGATTCCACAAAA  
GATGATAACTCCAACCCAGGAGGAAAGACAGATGAACCCAAAGGAAAACAGAAGCCTATTGGAAGC  
CATCAGAAAAAATTGAATGGTGAAGAAACATGACAAAAAAGGAAATAAGAAGATTATGACCTT  
CAAAGATGAGAGACTTCATCAATAAACAAAGCTGATGCTTATGTGGAGAAAAGGCATCCTTGACAAGGAA  
GAAGCCGAGGCCATCAAGCGCATTATAGCAGCCTGAAAATGGCAAAGATCCAGGAGTCTTCAA  
CTGTTTCAGAAAACATAATATAGCTAAAACACTTCAATTCTGTGATTAAAATTGGACCCAAAGG  
GTTATTAGAAAGTGTGAATTACAGTAGTTAACCTTTACAAGTGGTAAAACATAGCTTCTCCC  
GTAAAAACTATCTGAAAGTAAAGTTGTATGTAAGCTGAAAAAAAAAAAAAAAA

## **FIGURE 150**

MGFLGTGTWILVLVLPPIQAFPKPGGSQDKSLHNRELSAERPLNEQIAEAEEDKIKKTYPPENPG  
QSNSYSFVDNLNLLKAITEKEKIEKERQSIRSSPLDNKLNVEDVDSTKNRKLIDDYDSTKSGLDHK  
FQDDPDGLHQLDGTPLTAEDIVHKIAARIYEENDRAVFDFKIVSKLLNLGLITESQAHTLEDEVAE  
VLQKLISKEANNYEEDPNKPTSWTENQAGKIKEKVTMMAIQDGLAKGENDETVSNTLTLTNGL  
RRTKTYSEDNFEELQYFPNFYALLKSIDSEKEAKEKETLITIMKTLIDFVKMMVKYGTISPEEGV  
SYLENLDEMIALQTKNKLEKNATDNISKLFPAPSEKSHEETDSTKEEAAKMEKEYGSLKDSTKDD  
NSNPGGKTDEPKGKTEAYLEAIRKNIEWLKKHDKGKGNKEDYDLSKMRDFINKQADAYVEKGILD  
EEAEAIKRIYSSL

**N-glycosylation sites:**

amino acids 68-71, 346-349, 350-353

**Casein kinase II phosphorylation site:**

amino acids 70-73, 82-85, 97-100, 125-128, 147-150, 188-191, 217-  
220, 265-268, 289-292, 305-308, 320-323, 326-329, 362-365, 368-  
341, 369-372, 382-385, 386-389, 387-390

**N-myristoylation sites:**

amino acids 143-148, 239-244

## **FIGURE 151**

CGGCTCGAGGCTCCGCCAGGAGAAAGGAACATTCTGAGGGGAGTCTACACCCGTGGAGCTAA  
GATGGTCTGAGTGGGCGCTGTGCTCCGAATGAAGGACTCGGCATTGAAGGTGCTTTATCTGC  
ATAATAACCAGCTTCTAGCTGGAGGGCTGCATGCAGGGAAAGGTCAATTAAAGGTGAAGAGATCAGC  
GTGGTCCCCAATCGTGGCTGGATGCCAGCTGTCCCCGTCACTCTGGGTGTCCAGGGTGGAAAG  
CCAGTGCCTGTCAATGTGGGTGGGCAGGAGCCGACTCTAACACTAGAGCCAGTGAACATCATGG  
AGCTCTATCTGGTGCAGGAATCCAAGAGCTTCACCTTCTACCGCGGGACATGGGCTCACC  
TCCAGCTCGAGTCGGCTGCCTACCCGGCTGGTCTGTGCACGGTGCCTGAAGCCGATCAGCC  
TGTCAACTCACCCAGCTCCCGAGAATGGTGGCTGGAAATGCCCATCACAGACTTCACTTCC  
AGCAGTGTGACTAGGGCAACGTGCCCGAGAAGTCCCTGGGCAGAGCCAGCTCGGGTGGGG  
GAGTGGAGGAGACCCATGGCGGACAATCACTCTCTGTCTCAGGACCCCCACGTCTGACTTAG  
TGGGCACCTGACCACTTGTCTCTGGTCCAGTTGGATAAAATTCTGAGATTGGAGCTCACT  
CCACGGTCCTCCCCACTGGATGGTGCACTGCTGTGGAAACCTTGTAAAAACCATGTGGGTAAA  
CTGGGAATAACATGAAAAGATTCTGTGGGGGTGGGGGGGGAGTGGTGGGAATCATTCTGCT  
TAATGGTAACTGACAAGTGTACCTGAGCCCCGAGGCCAACCCATCCCCAGTGAGCCTTATA  
GGGTCAGTAGCTCCACATGAAGTCTGTCACTCACCACGTGCAGGAGAGGGAGGTGGTCATA  
GAGTCAGGGATCTATGGCCCTTGGCCCAGCCCCACCCCTTCAATCTGCCACTGTCA  
TGCTACCTTCTATCTTCCCTCATCATCTGTGTTGGCATGAGGAGGTGGTGTAGTCAGAA  
GAAATGGCTCGAGCTCAGAAGATAAAAGATAAGTAGGGTATGCTGATCCTTTAAAAACCAA  
GATACAATCAAATCCCAGATGCTGGTCTCTATTCCATGAAAAAGTGCTCATGACATATTGAGA  
AGACCTACTTACAAGTGGCATATATTGCAATTATTTAATTAAAGATAACCTATTATATT  
TCTTTATAGAAAAAGTCTGGAGAGTTACTCAATTGTAATTATCTGTATTCTCAATT  
AGGTGATTTCTTTAATTCTGTGTTAATTATCTGTATTCTCAATTCTCAATGAAGATGA  
ATTCTCTGTATAAAAATAAGAAAAGAAATTATCTGAGGTAAAGCAGAGCAGACATCATCTG  
TTGTCCTCAGCCTCCTACCTCCCCAGAGTAATTCAAATTGAATCGAGCTCTGCTGCTCTGGTGG  
TTGTTAGTAGTGTGAGCAAGATCTCAGCAAAGCCACTGAGGAGGGCTGTGCTGAGTTGT  
GTGGCTGGAAATCTCTGGTAAGGAACATAAGAACAAAATCATCTGGTAATTCTTCTAGAAG  
GATCACAGCCCCCTGGGATTCAAGGCATTGATCCAGTCTCTAAGAAGGCTGCTACTGGTGA  
ATTGTGCCCCCTCAAATTCACTCCTCTGGAAATCTCAGTCTGTGAGTTATTGGAGATAAG  
GTCTCTGAGATGTAGTTAGTTAGACAAGGTATGCTGAGGCTGAGGTTAGACCTAAATTCAATAT  
GACTGGTTCTGTATGAAAAGGAGAGGACACAGAGACAGAGGAGACGCCGGGAAGACTATGTA  
AAGATGAAGGCAGAGATCGGAGTTTGCAAGCCACAAGCTAAGAACACCAAGGATTGTGGCAACC  
ATCAGAACGTTGGAGAGGCAAAGAAGAATTCTCCCTAGAGGCTTAGAGGGATAACGGCTCTG  
CTGAAACCTTAATCTCAGACTTCCAGCCTCTGAACGAAGAAAGAATAATTCTGGCTTTAA  
GCCACCAAGGATAATTGGTTACAGCAGCTCTAGGAAACTAATACAGCTGCTAAATGATCCCTGT  
CTCCTCGTGTTCATTCTGTGTGTGCTCCCTCCACAATGTACCAAAGTTGTCTTGACCAA  
TAGAATATGGCAGAAGTGTGATGGCATGCCACTTCAAGATTAGGTTATAAAAGACACTGCA  
TACTTGAGCCCTCTCTCTGCCCCACCCACGGCCCCAATCTATCTGGCTACTCGCTCTGGGG  
AAGCTAGCTGCCATGCTATGAGCAGGCCATAAAAGAGACTTACGTGGTAAAAATGAAGTCTCCT  
GCCACAGCCACATTAGTGAACCTAGAAGCAGAGACTCTGTGAGATAATCGATTTGGTGT  
AAGTTGCTCAGTTGGCTAACTGTTATGCAAGATAAAATAATGCAAGAGAAAGAG

## **FIGURE 152**

MVLSGALCFRMKDSALKVLYLHNNQLLAGGLHAGKVIKGEIESVVPNRWLDASLSPVILGVQGGS  
QCLSCGVGQEPTLTLEPVNIMELYLGAKESKSFTFYRRDMGLTSSFESAAYPGWFLCTVPEADQP  
VRLTQLPENGGWNAPITDFYFQQCD

**N-myristylation sites.**

amino acids 29-34, 30-35, 60-65, 63-68, 73-78, 91-96, 106-111

**Interleukin-1 signature.**

amino acids 111-131

**Interleukin-1 proteins.**

amino acids 8-29, 83-120, 95-134, 64-103

## **FIGURE 153**

CTTCAGAACAGGTCTCCTCCCCAGTCACCAAGTTGCTCGAGTTAGAATTGTCTGCAATGGCCGC  
CCTGCAGAAATCTGTGAGCTTTCTTATGGGGACCCCTGGCCACCAGCTGCCTCTCTGG  
CCCTCTGGTACAGGGAGGAGCAGCTGCGCCATCAGCTCCACTGCAGGCTTAGCAAGTCCAAC  
TTCCAGCAGCCCTATATCACCAACCGCACCTCATGCTGGCTAAGGAGGCTAGCTGGCTGATAA  
CAACACAGACGTTCGTCTCATGGGAGAAACTGTTCCACGGAGTCAGTATGAGTGAGCGCTGCT  
ATCTGATGAAGCAGGTGCTGAACCTCACCCCTGAAGAAGTGCTGTTCCCTCAATCTGATAGGTT  
CAGCCTATATGCAGGAGGTGGTGCCTGGCCAGGCTCAGCAACAGGCTAAGCACATGTCA  
TATTGAAGGTGATGACCTGCATATCCAGAGGAATGTGCAAAAGCTGAAGGACACAGTGAAAAAGC  
TTGGAGAGAGTGGAGAGATCAAAGCAATTGGAGAACTGGATTGCTGTTATGCTCTGAGAAAT  
GCCTGCATTTGACCAGAGCAAAGCTGAAAAATGAATAACTAACCCCCCTTCCCTGCTAGAAATAA  
CAATTAGATGCCCAAAGCGATTTTTAACAAAAGGAAGATGGAAGCCTAACATCCATCATG  
ATGGGTGGATTCCAAATGAACCCCTGCGTTAGTTACAAAGGAAACCAATGCCACTTTGTTATA  
AGACCAGAAGGTAGACTTCTAAGCATAGATATTATTGATAACATTGTAACGGTGTTC  
TATACACAGAAAACAATTATTTTAAATAATTGTCTTTCCATAATCAGTACTTTATTTATAAA  
TCCTTAGGGAAAAAACCCCTAAATAGCTCATGTTCCATAATCAGTACTTTATTTATAAA  
TGTATTATTATTATTATAAGACTGCATTATTTATTCATTTATTAATATGGATTATT  
AGAAACATCATTGATATTGCTACTTGAGTGTAAGGCTAATATTGATATTATGACAATAATT  
AGAGCTATAACATGTTATTGACCTCAATAAACACTGGATATCCC

## **FIGURE 154**

MAALQKVSSFLMGTLATSCLLLALLVQGGAAAPISSHCRLDKSNFQQPYITNRTFMLAKEASL  
ADNNNTDVRLLIGEKLFHGVSMERCYLMQVLFNFTLEEVLFQSDRFQPYMQUEVVPFLARLSNRLS  
TCHIEGDDLHIQRNVQKLKDTVKKLGESGEIKAIGELDLLFMSLRNACI

**Important features of the protein:**

**Signal peptide:**

amino acids 1-33

**N-glycosylation sites.**

amino acids 54-58, 68-72, 97-101

**N-myristoylation sites.**

amino acids 14-20, 82-88

**Prokaryotic membrane lipoprotein lipid attachment site.**

amino acids 10-21

## **FIGURE 155**

GGCTTGCTGAAAATAAAATCAGGACTCCTAACCTGCTCCAGTCAGCCTGCTTCCACGAGGCCGT  
CAGTCAGTGCCGACTTGTGACTGAGTGTGCAGTGCAGCAGCATGTACCAGGTAGTCAGAGGGC  
TGCCTGAGGGCTGTGCTGAGAGGGAGAGGAGCAGAGATGCTGCTGAGGGTGGAGGGAGGCCAAGC  
TGCCAGGTTGGGCTGGGCAAGTGGAGTGGAGAAACTGGATCCCAGGGGAGGGTGCAGAT  
GAGGGAGCACCCAGATTAGGTGAGGACAGTTCTCATAGCCTTCTACAGGTGGTTGCAT  
TCTTGGCAATGGTCATGGAACCCACACCTACAGCCACTGGCCAGCTGCTGCCAGCAAAGGG  
CAGGACACCTCTGAGGAGCTGCTGAGGTGGAGCACTGTGCCTGTGCCCTAGAGCCTGCTAG  
GCCCAACCGCCACCCAGAGTCCTGTAGGGCCAGTGAAGATGGACCCCTAACAGCAGGGCCATCT  
CCCCCTGGAGATATGAGTTGGACAGAGACTGAAACCGGCTCCCCAGGACCTGTACCAACGCCGT  
TGCCTGTGCCCGACTGCGTCAGCCTACAGACAGGCTCCACATGGACCCCCGGGCAACTCGGA  
GCTGCTCTACCACAAACCAAGACTGCTTCTACAGGCGGCCATGCCATGGCGAGAAGGGCACCCACA  
AGGGCTACTGCCTGGAGCGCAGGCTGTACCGTGTTCCTAGCTTGTGTGTGCGGGCCCGT  
GTGATGGGCTAGCCGGACCTGCTGGAGGCTGGTCCCTTTGGGAAACCTGGAGGCCAGGTACA  
ACCACTTGCCTGAAGGGCCAGGATGCCAGATGCTTGGCCCTGTGAAGTGTCTGGAGCAG  
CAGGATCCCGGGACAGGATGGGGGCTTGGGAAAACCTGCACTTCTGCACATTGAAAAGAG  
CAGCTGCTGCTTAGGGCCGCCGGAAGCTGGTGTCTGTCTTCTCAGGAAAGGTTTCAA  
GTTCTGCCCATTCCTGGAGGCCACCACTCCCTGTCTTCCCTTTCCATCCCTGCTACCTG  
GCCCAGCACAGGCACTTCTAGATATTCCCCCTGCTGGAGAAGAAAGAGCCCCCTGGTTTATT  
TGTGTTGTTACTCATCACTCAGTGAGCATCTACTTGGGTGCATTCTAGTGTAGTTACTAGTCTT  
TTGACATGGATGATTCTGAGGAGGAAGCTGTTATTGAATGTATAGAGATTATCAAATAATAT  
CTTATTAATAAATGAAAAA

## **FIGURE 156**

MRERPRLGEDSSLISLFLQVVAFLAMVMGHTHTYSHWPSCCPGQDTSEELLRWSTVPVPPLEPA  
RPNRHPESCRASEDGPLNSRAISPWRYELDRDLNRLPQDLYHARCLCPHCVSLQTGSHMDPRGNS  
ELLYHNQTVFYRRPCHGEKGTHKGYCLERRLYRVSLACVCVRPRVMG

**Important features of the protein:**

**Signal peptide:**

amino acids 1-32

**N-glycosylation site.**

amino acids 136-140

**Tyrosine kinase phosphorylation site.**

amino acids 127-135

**N-myristylation sites.**

amino acids 44-50, 150-156

## **FIGURE 157**

CCGGCG**ATG**TCGCTCGTGTGCTAACGCTGGCCGCGCTGTGCAGGAGCGCCGTACCCCGAGAGCC  
GACCGTTCAATGTGGCTCTGAAACTGGGCCATCTCCAGAGTGGATGCTACAACATGATCTAACCC  
CCGGAGACTTGGAGGGACCTCCGAGTAGAACCTGTTACAACTAGTGTGCAACAGGGACTATTCA  
ATTTGATGAATGTAAGCTGGGTACTCCGGCAGATGCCAGCATCCGCTTGTGAAGGCCACCAA  
GATTTGTGTGACGGCAAAGCAACTTCCAGTCAGCTGTGAGGTGCAATTACACAGAGG  
CCTTCCAGACTCAGACCAGACCCCTGGTGGTAAATGGACATTTCTACATCGGCTTCCCTGTA  
GAGCTGAACACAGTCTATTCATTGGGCCATAATATTCTTAATGCAAATATGAATGAAGATGG  
CCCTTCATGTCTGTGAATTTCACCTCACCAGGCTGCCAGACATAATGAAATATAAAAAAA  
AGTGTGTCAAGGCCGAAGCCTGGGATCCGAAACATCACTGCTGTGAAAGAATGAGGAGACA  
GTAGAAGTGAACCTACAACCACTCCCTGGAAACAGATACTGGCTTATCCAACACAGCAC  
TATCATCGGTTTCTCAGGTGTTGAGCCACACCAGAAGAAACAAACGCGAGCTCAGTGGTGA  
TTCCAGTGAETGGGATAGTGAAGGTGCTACGGTGCAGCTGACTCCATATTCTACTTGTGGC  
AGCGACTGCATCCGACATAAGGAACAGTTGTGCTCTGCCACAAACAGGCGTCCCTTCCCTCT  
GGATAACAAACAAAGCAAGCCGGAGGCTGGCTGCCCTCCTGCTGTCTGCTGGTGGCCA  
CATGGGTGCTGGTGGCAGGGATCTATCTAATGTGGAGGCACGAAAGGATCAAGAAGACTCCCTT  
TCTACCACCAACTACTGCCCTCATTAAAGGTTCTGTGGTTACCCATCTGAAATATGTTCCA  
TCACACAATTGTTACTTCACTGAATTCTCAAAACCATTGCAAGTGAAGGTGAGGTCATCCTTGA  
AGTGGCAGAAAAGAAAATAGCAGAGATGGGTCCAGTGCAGTGGCTGCCACTCAAAGAAGGCA  
GCAGACAAAGTCGTTCCCTTCCAATGACGTCAACAGTGTGCGATGGTACCTGTGGCAA  
GAGCGAGGGCAGTCCAGTGAGAACTCTCAAGACCTTCCCTGCTTAAACCTTTCTGCA  
GTGATCTAAGAAGCCAGATTCTGACAAATACGTGGTGTACTTAGAGAGATTGATACA  
AAAGACGATTACAATGCTCTCAGTGTCTGCCCAAGTACCACCTCATGAAGGATGCCACTGCTT  
CTGTGCAGAACTCTCCATGTCAAGCAGCAGGTGTCAGCAGGAAAAAGATCACAAGCCTGCCACG  
ATGGCTGCTCCTTGT**AG**

## **FIGURE 158**

MSLVLLSLAALCRSAVPREPTVQCGSETGPSPEWMLQHDLIPGDLRDLRVEPVTTSVATGDYSILMNVS  
LRADASIRLLKATKICVTGKSNFQSYSCVRCNYTEAFQTQTRPSGGKWTFSYIGFPVELNTVYFIGAHHIP  
NANMNEDGPSMSVNFTSPGCLDHIMKYKKKCVKAGSLWDPNITACKNEETVEVNFTTPLGNRYMALIQH  
STIIGFSQVFEPHQKKQTRASVVIPTGDSSEGATVQLTPYFPTCGSDCIRHKGTVVLCPTGVPFPLDNNK  
SKPGGWLPLLLLSLLVATWVLVAGIYLMWRHERIKTSFSTTLLPPIKVLVVYPSEICFHHTICYFTEFL  
QNHCRCSEVILEKWQKKKIAEMGPVQWLATQKKAADKVVFLLSNDVNSVCDGTCGKSEGSPSENSQDLFPLA  
FNLFCSDLRSQIHLHKYVVVYFREIDTKDDYNALSVCPKYHLMKDATAFCAELLHVKKQQVSAGKRSQACHD  
GCCSL

**Important features of the protein:**

**Signal peptide:**

amino acids 1-14

**Transmembrane domain:**

amino acids 290-309

**N-glycosylation sites.**

amino acids 67 - 71, 103 - 107, 156 - 160, 183 - 187, 197 - 201 and 283  
- 287

**cAMP- and cGMP-dependent protein kinase phosphorylation sites.**

amino acids 228 - 232 and 319 - 323

**Casein kinase II phosphorylation sites.**

amino acids 178 - 182, 402 - 406, 414 - 418 and 453 - 457

**N-myristoylation site.**

amino acids 116-122

**Amidation site.**

amino acids 488-452

## **FIGURE 159**

AGCCACCAGCGAACATGACAGTGAAGACCC~~T~~GCATGGCCAGCCATGGTCAAGTACTTGCTGCT  
GTCGATATTGGGGCTTGCCTTCTGAGTGAGGCGGCAGCTGGAAAATCCCAAAGTAGGACATA  
CTTTTTCCAAAAGCCTGAGAGTTGCCGCCTGTGCCAGGAGGTAGTATGAAGCTTGACATTGGC  
ATCATCAATGAAAACCAGCGCTTCCATGTCACGTAACATCGAGAGCCGCTCCACCTCCCCCTG  
GAATTACACTGTCACTTGGGACCCCAACC~~GGT~~TACCCCTCGGAAGTTGTACAGGCCAGTGTAGGA  
ACTTGGGCTGCATCAATGCTCAAGGAAAGGAAGACATCTCCATGAATTCCGTTCCATCCAGCAA  
GAGACCC~~T~~GGTCGTCGGAGGAAGCACCAAGGCTGCTCTGTTCTTCCAGTTGGAGAAGGTGCT  
GGTGA~~C~~TTGGCTGCACCTGCGTCACCC~~T~~GTCATCCACCATGTGCAGTAAGAGGTGCATATCC  
ACTCAGCTGAAGAAG

## **FIGURE 16O**

MTVKTLHGPAMVKYLLSILGLAFLSEAARKIPKVGHFFQKPESCPPVPGGSMKLDIGIINEN  
QRVMSMRNIESRSTSPWNYTVWDPNRYPSEVVQAQCRLGCINAQGKEDISMNSVPIQQETLVV  
RRKHQGCSVSFQLEKVLVTVGCTCVTPVIHHVQ

**Signal sequence:**

amino acids 1-30

**N-glycosylation site.**

amino acids 83-87

**N-myristoylation sites.**

amino acids 106-111, 136-141

## **FIGURE 161**

ACACTGGCAAACAAAAACGAAAGCACTCCGTGCTGGAAGTAGGAGGAGACTCAGGACTCCAGG  
ACAGAGAGTGCACAAACTACCCAGCACAGCCCCCTCCGCCCCCTGGAGGCTGAAGAGGGATT  
CAGCCCCCTGCCACCCACAGACACGGGCTGACTGGGTGCTGCCCCCTGGGGGGGGCAC  
AGGGCCTCAGGCCTGGGTGCCACCTGGCACTAAGAAGATGCTGTGCCCTGGTCTGCTGC  
TGGCACTGGGCCAGGCCAGTGGCTTCTCTGGAGAGCTTGTGGGCCCTAGGACGTAC  
CACTGCTCTCCGGGCCCTCTCCTGCCGCTCTGGGACAGTGACATACTCTGCCCTGGGAC  
CGTGCCTGCTCCGGGCCGTGCTGGCGCTACGCACCTGCAGACAGACTGCTGCTGAGTG  
AGAAGGAGACCGACTGTGACCTCTGCTGCGTGTGGCTGTCCACTTGGCCTGCACTGG  
GAAGAGCCTGAAGATGAGGAAAAGTTGGAGGAGCAGCTGACTCAGGGTGGAGGACCTAG  
TGCCTCTCCAGGGCCAAGTCGTGCTCTCCTCCAGGCCACCCACTGCCCTGCTGCTC  
TGGAGGTGCAAGTGCCTGCTGCCCTTGTGCAAGTGGTCACTGTGGCTCTGGTATATG  
TGCTTCGAGGCTGCCCTAGGGATGAGGTACGAATCTGGTCTTACTCAGCCAGGTAC  
GAGAAGACTCAACCACACAGACACTGCCCTGCCCTGGCTAACGTGTCAGCAGATGGT  
ACGTGCATCTGGTTCTGAATGTCCTGAGGAGCAGCACTCCGGCTCTCCGTACTGGA  
GTCCAGGGCCCCAAAACCCGGTGGCACAAAAACCTGACTGGACCGCAGATCATTAC  
CCACACAGACCTGGTCCCTGCCTCTGATTCAAGGTGTCAGGACTCCGGTTAGGA  
CGAACATCTGCCCTCAGGGAGGACCCCGCGCACACCAGAACCTCTGGCAAGCC  
CGACTGCTGACCTGCAGAGCTGGTCTGGACGCACCGTGTGCTGCCGCGAGAAGCG  
GTGCTGGCGGGCTCCGGTGGGACCCCTGCCAGCCACTGGTCCACCGCTTCTGG  
TCACGTGGACAAGTTCTCGAGTTCCCATGCTGAAAGGCCACCCCTAAC  
AACAGCTCGGAGAAGCTGCAGCTGCAGGAGTGCTGTGGCTGACTCCCTGG  
CGATGTGCTACTGTGGAGACACGAGGCCAGGACAACAGATCCCTCTGTGG  
GTGGCTGACTTCACTACCCAGCAAAGCCTCACGAGGGCAGCTGCCCTGG  
CAAGACCTGCACTGGCAGTGTCTGCAGCTATGGACGATGACTTGG  
CCCCATGGACAAATACATCCACAAGCGCTGGGCCCTCGTGTGGCTG  
CTGCGCTTCCCTCATCCTCTCAAAAAGGATCACCGCAGGACTT  
CAGGACGTCCGCTCGGGGGGGGGGGGGGGGGGGGGGGGGGG  
CTCGGGTTTCGAGGCCCTGGTGGCGCCCTGGCGTGGGCCCTGT  
CCGTAGACCTGTGGAGCCGTGAACTGAGCGCAGGGGGGG  
CGGCAGCAGACCTGCAGGAGGGCGGTGGTGTCTTCT  
GTGAGCTGGCTACAGGATGGGTGTCCGGGCCGGGGCG  
GCGCCTCGCTCAGCTGCGTGTGCCGACTTCTGCA  
GCCTGCTTCGACAGGCTGCTAACCGGACGCCGT  
CACACTGCCCTCCCAACTGCCAGACTTCTGGGGCC  
GGCGGCTCCAAGAGAGAGCGGAGCAAGTGT  
CATCCCCGGGACTCCCGCGCCGGACGCCGGGG  
CGGGACTTAATAAAGCAGACGCTGTTTCTAAAAAA

## **FIGURE 162**

MPVPWFLLSLALGRSPVVLSLERLVPQDATHCSPGLSCRWDSDLCLPGDIVPAPGPVLAPTHLQTELVLRCQKETDCDLCLRVAVHLAVHGHWEPEDEEKGGAADSGVEEPRNASLQAQVVLSFQAYPTARCVILLEVQVPAALVQFGQSVGSVYDCFEAALGSEVRIWSYTQPRYEKELNHTQQLPALPWLNVSADGDNVHLVNVSEEQHFGLSLYWNQVQGPPKPRWHKNLTGPQIITLNHTDLVPCLCIQVWPLEPDSVRTNICPFREDPRAHQNLWQAARLRLTLQSWLLDAPCSLPAEAALCWRAPGGDPCQPLVPPLSWENVTVDKVLFPPLLKGHPNLCVQVNSSEKQLQCLWADSLGPLKDDVLLLETRGPQDNRSLCALEPSGCTSILPSKASTRAARLGEYLLQDLQSGQCLQLWDDDLGALWACPMDKYIHKRWALVWLACLLFAAALSLLLLKKDHAKGWLRLKQDVRSGAAARGRAALLLYSADDGFERLVGALASALCQLPLRVADLWSRRELSAQGPVAWFHAQRRQTLQEGGVVVLLFSPGAVALCSEWLQDGVSQPGGAHGPDAFRASLSCVLPDFLQGRAPGSYVGACFDRLLHPDAVPALFRTVPVFTLPSQLPDFLQPRAPRSGRLQERAEQVSRALQPALDSYFHPPGTPAPGRGVGPGAGPGAGDGT

**Signal sequence:**

amino acids 1-20

**Transmembrane domain.**

amino acids 453-475

**N-glycosylation sites.**

amino acids 118-121, 186-189, 198-201, 211-214, 238-241, 248-251, 334-337, 357-360, 391-394

**Glycosaminoglycan attachment site.**

amino acids 583-586

**cAMP- and cGMP-dependent protein kinase phosphorylation site.**

amino acids 552-555

**N-myristoylation sites.**

amino acids 107-112, 152-157, 319-324, 438-443, 516-521, 612-617, 692-697, 696-701, 700-705

## FIGURE 163

GGGAGGGCTCTGTGCCAGCCCCGATGAGGACGCTGTGACCATTTGACTGTGGGATCCCTGGCT  
GCTCACGCCCTGAGGACCCCTCGGATCTGCTCCAGCACGTGAAATTCCAGTCAGCAACTTGA  
AAACATCCTGACGTGGACAGGGCCAGAGGGCACCCAGACACGGTCTACAGCATCGAGTATA  
AGACGTACGGAGAGAGGGACTGGGTGCAAAGAAGGGCTGCAGGGATCACCCGGAAAGTCCCTGC  
AACCTGACGGTGGAGACGGGCAACCTCACGGAGCTCTACTATGCCAGGGTACCCGCT  
GTCAGTGCAGGGAGGGCGGTCAAGCACCAGATGACTGCAGGGTCAGCTCTGCAGCACACTAC  
CCTCAAGCCACCTGATGTGACCTGTATCTCCAAAGTGAAGATCGATTAGATGATTGTCATCCTA  
CCCCCACGCCAATCCGTGCAGGGCATGGCCACCCGGCTAACCCCTGGAAGACATCTTCCATGACCTG  
TTCTACCACTTAGAGCTCCAGGTCAACCGCACCTACCCAAATGCACCTTGGAGGGAAAGCAGAGAGA  
ATATGAGTTCTCGGCCTGACCCCTGACACAGAGTTCCCTGGCACCATCATGATTGCGTTCCCA  
CCTGGGCAAGGAGAGTGCCTTACATGTGCCAGTGAAGACACTGCCAGACGGGACATGGACC  
TAATCCCTCTCGGAGCCTTCTGTGTTCTCCATGGGCTTCTGTCGCGAGTACTCTGCTACCTGAG  
CTACAGATATGTCACCAAGCCGCTGCACCTCCAACTCCCTGAACTGTCAGCGAGTCTGACTT  
TCCAGCCGCTGCGCTTCATCCAGGAGCACGTCTGTTCTGACCTCAGCGGGCCCCAGC  
AGTCTGGCCAGGCTGTCAGTACTCCCAGATCAGGGTGTCTGGACCCAGGGAGCCGAGGAGC  
TCCACAGCGGCATAGCCTGTCGAGATCACCTACTTAGGGCAGGCCAGACATCTCATCCTCCAGC  
CCTCCAACGTGCCACCTCCCCAGATCCTCTCCCCACTGTCTATGCCCAAAAGCCTGCCCTGAG  
GTCGGGCCCCATCTATGCACCTCAGGTGACCCCCGAAGCTCAATTCCATTCTACGCCAAC  
GCCATCTAAGGCCAGCCTCCTCTATGCCCTCAAGCCACTCCGGACAGCTGGCTCCCT  
CCTATGGGTATGCACTGGAAAGGTTCTGGCAAGAGACTCCCCACTGGGACACTTCTAGTCTAA  
CACCTTAGGCCTAAAGGTCACTGGCTAGAAAGGCCACAGCTGGAAAGCTGCAATTGACCCAGC  
TTCTCTGCAAGGAGGTGACCTCTGGCTATGGAGGAATCCCAAGAAGCAAATCATTGACCCAGC  
CCCTGGGATTTCACAGACAGAACATCTGACCCAAATGTCTACACAGTGGGAGGAAGGGAC  
CCACAGTACCTAAAGGGCCAGCTCCCCCTCCCTCTCCTAGCTCAGGAGGGCCACCCATGTC  
CCTCCCCCTGCAACTCCTTCCGGTCCATGTTCCCCCTGGACCAAGGTCCAAGTCCCTGGGCC  
TGCTGGAGTCCCTTGTGTGCTCAAGGATGAAGCCAAGAGGCCACGGGCTGAGACCTCAGACCTG  
GAGCAGCCCACAGAACATGGATTCTCTTCAAGGCCCTGGGCTGACTGTGCAATTGGAGTCTG  
AGGGGAATGGGAAAGGCTGGTCTCTCCCTGCTCCATCCCAGTGTCACTATCTGGCTGTCA  
ATCCCATGCTGCCCATGCCACACTCTGCACTGGCCTCAGACGGGTGCCCTGAGAGAAC  
AGAGGGAGTGGCATGCCAGGGCCCTGCATGGTGCCTCCAGGGAAACAAGCAGCATGATA  
AGGACTGCAAGGGGGAGCTCTGGGAGCAGCTGTGAGACAAAGCGCTGCTCGTGCAGCC  
CAAGGCAGAAATGACAGTCAAGGAGGAATGCAAGGGAAACTCCCGAGGTCCAGAGCCCCACCTC  
CTAACACCATGGATCAAAGTCTCAGGGAAATTGCTCTGCCCTCTCTGTCATTGTCATTGGCAAG  
ACAATCTAGCTCGACAGAGCATGAGGCCCTGCCCTCTGTCATTGTCATTGGCAAG  
GCCTGGAAAAGAACCAAGGCCCTGGAAAAGAACAGAACAGAACAGGAGGCTGGCAGAAC  
ACTTCTGCCAAGGCCAGGGCCAGCAGGACGGCAGGACTCTAGGGAGGGGTGTGGCCTGCAGCTCA  
TTCCCAAGCCAGGGCAACTGCCTGACGTTGCACTGATTTCTGTCAGCTTCTGTCAG  
GAAATGCAAGGTCCACCAGGGAGGGAGACACACAAGCCTTTCTGCAAGGAGGTTTCAGACCC  
ATCCTGAGAATGGGGTTGAAAGGAAGGTGAGGGCTGTCAGGGCTGGGCCATGGTACAATAACAC  
TGTACTGATGTCAACACTTGCAGCTCTGCCCTGGGTCAAGGCCCTGTCAGGGCTCAAAATTCCAGC  
CTCACCACTCACAAGCTGTGTGACTTCAAACAAATGAAATCAGTGCAGGGCAACCTCGGTTCC  
ATCTGTAATGTGGGGATCATAACACACTACCTCATGGAGTTGTGGTGAAGATGAAATGAAGT  
TCTTTAAAGTGTCTTAATAGTGCCTGGTACATGGGCAAGTGCCTAAACGGTAGCTATTTAAAAA  
AAAAAAA

## **FIGURE 164**

MRTLLTILTGVSLAAHAPEDPSDLLQHVKFQSSNFENILTWDSGPEGTPDTVYSIEYKTYGERDW  
VAKKGCQRITRKSCNLTVEGNLTLYYARVTAVSAGGRSATKMTDRFSSLQHTTLKPPDVT CIS  
KVRSIQMIVHPTPTPIRGDGHLTLIEDIFHDLFYHLELQVNRTYQMHLGGKQREYEFFGLTPDT  
EFLGTIMICVPTWAKESAPYMCRVKTLPDRTWTYSFSGAFLFSMGFLVAVLCYLSYRYVTKPPAP  
PNSLNQVRVLTQPLRFIQEHVLIPVFDLSGPSSLAQPVQYSQIRVSGPREPAGAPQRHSLSEIT  
YLGQPDISILQPSNVPPPQILSPLSYAPNAAPEVGPPSYAPQVTPEAQFPFYAPQAISKVQPSSY  
APQATPDSWPPSYGVCMEGSGKDSPTGTLSSPKHLRPKGQLQKEPPAGSCMLGGLSLQEVTSLAM  
EESQEAKSLHQPLGICTDRTSDPNVLHSGEEGTPQYLKGQLPLLSSVQIEGHPMSLPLQPPSGPC  
SPSDQGPSPWGLLESLVCPKDEAKSPAPETSDEQPTELDSLFRGLALTQWES

**Signal sequence.**

amino acids 1-17

**Transmembrane domain.**

amino acids 233-250

**N-glycosylation sites.**

amino acids 80-83, 87-90, 172-175

**N-myristoylation sites.**

amino acids 11-16, 47-52, 102-107, 531-536, 565-570

## **FIGURE 165**

TGGCCTACTGGAAAAAAAAAAAAAAAAAAGTCACCCGGGCCCCGGTGGCCACAACATGG  
CTGCGGCGCCGGGGCTGCTCTTCTGGCTGTCGTGGCTGGGGCGCTGGTGGTCCCGGCAG  
TCGGATCTCAGCCACGGACGGCGTTCTGGACCTCAAAGTGTGGGGGACGAAGAGTCAGCAT  
GTTAATGTACCGTGGAAAGCTTGAAGACTTCACGGGCCCTGATTGTCGTTGTGAATTAA  
AAAAAGGTGACGATGTATATGCTACTACAAACTGGCAGGGGGATCCCTGAACTTGGGCTGGA  
AGTGGTGAACACAGTTGGATATTTCCAAAAGATTGATCAAGGTACTTCATAAATACCGGA  
AGAAGAGCTACATATTCCAGCAGATGAGACAGACTTGTCTGCTTGAAGGAGGAAGAGATGATT  
TTAATAGTTATAATGAGAAGAGCTTTAGGATCTTGGAACTGGAGGACTCTGTACCTGAAGAG  
TCGAAGAAAGCTGAAGAAGTTCTCAGCACAGAGAGAAATCTCTGAGGAGTCTCGGGGGCGTGA  
ACTTGACCTGTGCCTGAGCCCAGGGCATTCAGAGCTGATTCAAGGGATGGAGAAGGTGCTTCT  
CAGAGAGCACCGAGGGGCTGCAGGGACAGCCCTCAGCTCAGGAGAGCCACCCACACCAGCGGT  
CCTGCGGCTAACGCTCAGGGAGTGCAGTCTCGTTGGACACTTGAAGAAATTCTGCACGATAA  
ATTGAAAGTGCCGGAAAGCAGAAAGCAGAACTGGCAATAGTTCTCCTGCCTCGGTGGAGCGGGAGA  
AGACAGATGCTTACAAAGTCCTGAAAACAGAAATGAGTCAGAGAGGAAGTGGACAGTGCCTTATT  
CATTACAGCAAAGGATTCGTTGGCATCAAATCTAAGTTGTTACAAAGATTGTTTAGTA  
CTAAGCTGCCCTGGCAGTTGCATTGAGCAAACAAAAATATAATTATTTCCCTCTAAGTA  
AAAAAAAAAAAAAAAAA

## **FIGURE 166**

MAAAPGLLFWLFVLGALWWVPGQSDLSHGRRFSDLKVCGLDEECMMLMYRGKALEDFTGPDCRFVN  
FKKGDDVYVYYKLAGGSLELWAGSVEHSFGYFPKDLIKVLHKYTEEELHI PADETDFVCFEGGRD  
DFNSYNVEELLGSLELEDSPVPEESKKAAEVSQHREKSPPEESRGRELDPVPEPEAFRADSEDEGEGA  
FSESTEGLQGQPSAQESHPHTSGPAANAQGVQSSLDTFEEILHDKLKVPGSESRTGNSSPASVER  
EKTDAYKVLKTEMSQRGSGQCVIHYSKGFRWHQNLSLFYKDCF

**Important features of the protein:**

**Signal peptide:**

amino acids 1-22

**N-glycosylation site.**

amino acids 294-298

**cAMP- and cGMP-dependent protein kinase phosphorylation site.**

amino acids 30-34

**Tyrosine kinase phosphorylation site.**

amino acids 67-76

**N-myristoylation sites.**

amino acids 205-211, 225-231, 277-283

**Amidation site.**

amino acids 28-32

## **FIGURE 167**

CCAGGACCAGGGCGCACCGGCTCAGCCTCTCACTGTCAGAGGCCGGGAAGAGAAGCAAAGCGC  
AACGGTGTGGTCCAAGCCGGGCTCTGCTCGCCTCTAGGACATAACAGGGACCCCTAACCTC  
AGTCCCCAAACGCGCACCCCTCGAAGTCTTAACTCCAGCCCCGACATCCACCGCGGGCACAGG  
CGCGGCAGGCGGCAAGGTCCCAGGCGAAGGGATGCGCGCAGGGGTCGGGCAGCTGGCTCGGGC  
GGCAGGGAGTAGGGCCCGGCAGGGAGGCAGGGAGGCTGCATATTCAAGAGTCGCGGGCTGCGCCCTG  
GGCAGAGGCCGCCCTCGCTCCACGCAACACCTGCTGCTGCCACCGCGCGCAGTGAGCCGCGTGG  
TCTCGCTGCTGCTGGCGCCGCTGCTGCTGCCACGGAGCCTCTGCGCGCGTGGTCAGC  
GGCCAAAAGGTGTGTTTGCTCACTCAACATCCTGCTACAAAATGGCTACTTCCATGAAC  
GTCCAGCCGAGTGAAGCTTCAGGAGGCCCTGCTGTTGAGAGTGAGGGAGGAGTCCTCTCA  
GCCTGAGAATGAAGCAGAACAGAAGTTAAGAGACATGTTGCAAAACCTGACAAAACCGGG  
ACAGGGATTCTGATGGTGAATTCTGGATAGGGTTGGAGAATGGAGATGGCAAACATCTGG  
TGCCTGCCAGATCTTACCACTGCTGATGGAAGCAATTCCCAGTACCGAAACTGGTACACAG  
ATGAACCTCTGGAAGTGAAGAAGTGAACAACTGCAACTGCCAATCTGG  
CTTGGGGTCCCTACCTTACCACTGTTGAGAATGATGACAGGTGTAACATGAAGCACAATTATTTG  
CAAGTATGAACCAGAGATTAATCCAACAGCCCTGAGAAAAGCCTTATCTAACAAATCAACCAG  
GAGACACCCATCAGAATGTTGAGTGAAGCAGGTATAATTCCAATCTAATTATGTT  
ATACCAACAATACCCCTGCTCTACTGATACTGGTTGCTTGGAAACCTGTTCCAGATGCT  
GCATAAAAGTAAAGGAAGAACAAAAGTCAACTGCAAACCCAGTCTACACTGTGGATTCAAAGAGTA  
CCAGAAAAGAAAGTGGCATGGAAGTATAACTCATGACTTGGTCCAGAATTGTAATTCT  
GGATCTGTATAAGGAATGGCATCAGAACAAATAGCTTGGGAATGGCTGAAATCAAAGGATCTGC  
AAGATGAACTGTAAGCTCCCCCTGAGGCAAATATTAAAGTAATTTTATATGCTATTATTC  
TTTAAAGAATATGCTGCTAAATAATGGAGTGAGACATGCTTATTGCTAAAGGATGCACCCAA  
ACTTCAAACTCAAGCAAATGGAATGGCAATGCAAGATAAAGTGTATCAACACGTGGAGTA  
TGTGTGTTAGAAGCAATTCTTTATTCTTCACCTTCTCAAGTTGTTACGTCAATGTA  
TGTATATTGTTGAAATTACAGTGTGCAAAGTATTTCACCTTGCATAAGTGTGATAAAA  
ATGAACCTGTTCTAAATATTATTGTCATCTCATTTCATAACATGCTCTTGTGATAAAG  
AAACTTAACTACTGTTGCAACTGAAATTCAACACACACAAATATAGTACCATAGAAAAAGTTGT  
TTTCTCGAAATAATTCTTCAGCTCTGCTTGGTCAAGTCTAGGAATCTTCAGA  
ATAAGAAGCTATTCTAAAGTGTGATAAAACCTCTCAAACATTACTAGGCAAGGAT  
TGTCTAAATTCAATTGTGCAAGACATGTGCTTATAATTATTAGCTTAAATTAAACAGATT  
TTGTAATAATGTAACTTGTTAATAGGTGATAAACACTAATGCAATTGAAACAAAAGAAG  
TGACATACACAATATAAATCATATGCTTCACACGTTGCTTATATAATGAGAAGCAGCTCTGA  
GGGTTCTGAAATCAATGTTGGCCCTCTGCCCCACTAAACAAAGATGGTTGTCGGGTTGG  
ATTGACACTGGAGGCAGATAGTTGCAAAGTTAGTCTAAGGTTCCCTAGCTGTTAGCTCTG  
ACTATATTAGTACAAAGAGGTATGTGTTGAGACAGGGTAATAGTCACTATCAGTGTGGAG  
ACAAGCACAGCACACAGACATTAGGAAGGAAGGAACATCGAAATCGTGTGAAATGGGTTGG  
AACCCATCAGTGATCGCATATTCAATTGATGAGGGTTGCTTGAGATAGAAAATGGGCTCCTT  
CTGTCTTATCTCTAGTTCTCAATGCTACGCCCTGTTCTCAAGAGAAAGTTGTAACCT  
CTGGTCTTCAATGTCCTGCTCCTTAAACCAATAAGAGTCTTGTGTTCTGGGGAAAAAA  
AAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAA

## **FIGURE 168**

MSRVVSLLLGAALLCGHGAFCRVVSGQKVCADFHKPCYKMAFHELSSRVSFQEARNLACESE  
GGVLLSLENEAEQKLIIESMLQNLTKPGTGISDGDFWIGLWRNGDGOTSGACPDLQWSDGSNSQ  
YRNWYTDEPSCGSEKCVVMYHQPTANPGLGGPYLYQWNDDRCNMKHNYICKYEPEINPTAPVEK  
PYLTNQPGDTHQNVVTEAGIIPNLIYVVIPTIPLLLLILVAFGTCCFQMLHKSKGRTKTSPNQ  
STLWISKSTRKESGMEV

**Important features of the protein:**

**Signal peptide:**

amino acids 1-21

**Transmembrane domain:**

amino acids 214-235

**N-glycosylation sites.**

amino acids 86-89, 255-258

**cAMP- and cGMP-dependent protein kinase phosphorylation site.**

amino acids 266-269

**N-myristoylation sites.**

amino acids 27-32, 66-71, 91-96, 93-98, 102-107, 109-114, 140-145, 212-217